

“ ”

• }
|||

67

515

419

371

323

275

221

60

ccacgcgtcc	ggccttcgga	aatagaaaaca	aagttgggtca	caaattcacat	tagcttttgcc	60
cgaagttttt	ccccacactc	ttcttttagca	tgctattatg	gggaaagtga	ccactcctgg	120
gagcgggggt	ggtcggggcg	gtttgggtggc	ggggaagcgg	ctgtaacttc	tacgtgacc	179
atg gta cct gtt gaa aac acc gag ggc ccc agt	ctg ctg aac cag aag	227				
Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser	Leu Leu Asn Gln Lys					
1	5	10	15			
ggg aca gcc gtg gag acg gag ggc agc ggc agc cgg cat cct ccc tgg	275					
Gly Thr Ala Val Glu Thr Glu Gly Ser Gly Ser Arg His Pro Pro Trp						
	20	25	30			
gcg aga ggc tgc ggc atg ttt acc ttc ctg tca tct gtc act gct gct	323					
Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Thr Ala Ala						
	35	40	45			
gtc agt ggc ctc ctg gtg ggt tat gaa ctt ggg atc atc tct ggg gct	371					
Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala						
	50	55	60			
ctt ctt cag atc aaa acc tta tta gcc ctg agc tgc cat gag cag gaa	419					
Leu Leu Gln Ile Lys Thr Leu Leu Ala Leu Ser Cys His Glu Gln Glu						
	65	70	75	80		
atg gtt gtg agc tcc ctc gtc att gga gcc ctc ctt gcc tca ctc acc	467					
Met Val Val Ser Ser Leu Val Ile Gly Ala Leu Leu Ala Ser Leu Thr						
	85	90	95			
gga ggg gtc ctg ata gac aga tat gga aga agg aca gca atc atc ttg	515					

Gly 100	Gly 101	Val 102	Leu 103	Ile 104	Asp 105	Arg 106	Tyr 107	Gly 108	Arg 109	Arg 110	Thr 111	Ala 112	Ile 113	Ile 114	Leu 115	
tca Ser	tcc Ser	tgc Cys 115	ctg Leu	ctt Leu	gga Gly	ctc Leu	gga Gly 120	agc Ser	tta Leu	gtc Val	ttg Leu	atc Ile 125	ctc Leu	agt Ser	tta Leu	563
tcc Ser	tac Tyr 130	acg Thr	gtt Val	ctt Leu	ata Ile	gtg Val 135	gga Gly	cgc Arg	att Ile	gcc Ala	ata Ile 140	ggg Gly	gtc Val	tcc Ser	atc Ile	611
tcc Ser 145	ctc Leu	tct Ser	tcc Ser	att Ile	gcc Ala 150	act Thr	tgt Cys	gtt Val	tac Tyr	atc Ile 155	gca Ala	gag Glu	att Ile	gct Ala	cct Pro 160	659
caa Gln	cac His	aga Arg	aga Arg	ggc Gly 165	ctt Leu	ctt Leu	gtg Val	tca Ser	ctg Leu 170	aat Asn	gag Glu	ctg Leu	atg Met 175	att Ile	gtc Val	707
atc Ile	ggc Gly	att Ile	ctt Leu 180	tct Ser	gcc Ala	tat Tyr	att Ile	tca Ser 185	aat Asn	tac Tyr	gca Ala	ttt Phe	gcc Ala 190	aat Asn	gtt Val	755
ttc Phe	cat His	ggc Gly 195	tgg Trp	aag Lys	tac Tyr	atg Met	ttt Phe 200	ggt Gly	ctt Leu	gtg Val	att Ile	ccc Pro 205	ttg Leu	gga Gly	gtt Val	803
ttg Leu	caa Gln 210	gca Ala	att Ile	gca Ala	atg Met	tat Tyr 215	ttt Phe	ctt Leu	cct Pro	cca Pro	agc Ser 220	cct Pro	cgg Arg	ttt Phe	ctg Leu	851
gtg Val 225	atg Met	aaa Lys	gga Gly	caa Gln	gag Glu 230	gga Gly	gct Ala	gct Ala	agc Ser	aag Lys 235	gtt Val	ctt Leu	gga Gly	agg Arg	tta Leu 240	899
aga Arg	gca Ala	ctc Leu	tca Ser	gat Asp 245	aca Thr	act Thr	gag Glu	gaa Glu	ctc Leu 250	act Thr	gtg Val	atc Ile	aaa Lys	tcc Ser 255	tcc Ser	947
ctg Leu	aaa Lys	gat Asp 260	gaa Glu	tat Tyr	cag Gln	tac Tyr	agt Ser	ttt Phe 265	tgg Trp	gat Asp	ctg Leu	ttt Phe	cgt Arg 270	tca Ser	aaa Lys	995
gac Asp	aac Asn 275	atg Met	cgg Arg	acc Thr	cga Arg	ata Ile	atg Met 280	ata Ile	gga Gly	cta Leu	aca Thr	cta Leu 285	gta Val	ttt Phe	ttt Phe	1043
gta Val	caa Gln 290	atc Ile	act Thr	ggc Gly	caa Gln	cca Pro 295	aac Asn	ata Ile	ttg Leu	ttc Phe	tat Tyr 300	gca Ala	tca Ser	act Thr	gtt Val	1091
ttg Leu 305	aag Lys	tca Ser	gtt Val	gga Gly	ttt Phe 310	caa Gln	agc Ser	aat Asn	gag Glu	gca Ala 315	gct Ala	agc Ser	ctc Leu	gcc Ala	tcc Ser 320	1139
act Thr	ggg Gly	gtt Val	gga Gly	gtc Val 325	gtc Val	aag Lys	gtc Val	att Ile	agc Ser 330	acc Thr	atc Ile	cct Pro	gcc Ala 335	act Thr	ctt Leu	1187
ctt Leu	gta Val	gac Asp	cat His	gtc Val	ggc Gly	agc Ser	aaa Lys	aca Thr	ttc Phe	ctc Leu	tgc Cys	att Ile	ggc Gly	tcc Ser	tct Ser	1235

340										345					350					
gtg	atg	gca	gct	tcg	ttg	gtg	acc	atg	ggc	atc	gta	aat	ctc	aac	atc	1283				
Val	Met	Ala	Ala	Ser	Leu	Val	Thr	Met	Gly	Ile	Val	Asn	Leu	Asn	Ile					
355							360					365								
cac	atg	aac	ttc	acc	cat	atc	tgc	aga	agc	cac	aat	tct	atc	aac	cag	1331				
His	Met	Asn	Phe	Thr	His	Ile	Cys	Arg	Ser	His	Asn	Ser	Ile	Asn	Gln					
370					375					380										
tcc	ttg	gat	gag	tct	gtg	att	tat	gga	cca	gga	aac	ctg	tca	acc	aac	1379				
Ser	Leu	Asp	Glu	Ser	Val	Ile	Tyr	Gly	Pro	Gly	Asn	Leu	Ser	Thr	Asn					
385			390					395					400							
aac	aat	act	ctc	aga	gac	cac	ttc	aaa	ggg	att	tct	tcc	cat	agc	aga	1427				
Asn	Asn	Thr	Leu	Arg	Asp	His	Phe	Lys	Gly	Ile	Ser	Ser	His	Ser	Arg					
405					410					415										
agc	tca	ctc	atg	ccc	ctg	aga	aat	gat	gtg	gat	aag	aga	ggg	gag	acg	1475				
Ser	Ser	Leu	Met	Pro	Leu	Arg	Asn	Asp	Val	Asp	Lys	Arg	Gly	Glu	Thr					
420				425					430											
acc	tca	gca	tcc	ttg	cta	aat	gct	gga	tta	agc	cac	act	gaa	tac	cag	1523				
Thr	Ser	Ala	Ser	Leu	Leu	Asn	Ala	Gly	Leu	Ser	His	Thr	Glu	Tyr	Gln					
435			440					445												
ata	gtc	aca	gac	cct	ggg	gac	gtc	cca	gct	ttt	ttg	aaa	tgg	ctg	tcc	1571				
Ile	Val	Thr	Asp	Pro	Gly	Asp	Val	Pro	Ala	Phe	Leu	Lys	Trp	Leu	Ser					
450			455					460												
tta	gcc	agc	ttg	ctt	gtt	tat	gtt	gct	gct	ttt	tca	att	ggt	cta	gga	1619				
Leu	Ala	Ser	Leu	Leu	Val	Tyr	Val	Ala	Ala	Phe	Ser	Ile	Gly	Leu	Gly					
465			470					475					480							
cca	atg	ccc	tgg	ctg	gtg	ctc	agc	gag	atc	ttt	cct	ggt	ggg	atc	aga	1667				
Pro	Met	Pro	Trp	Leu	Val	Leu	Ser	Glu	Ile	Phe	Pro	Gly	Gly	Ile	Arg					
485					490					495										
gga	cga	gcc	atg	gct	tta	act	tct	agc	atg	aac	tgg	ggc	atc	aat	ctc	1715				
Gly	Arg	Ala	Met	Ala	Leu	Thr	Ser	Ser	Met	Asn	Trp	Gly	Ile	Asn	Leu					
500				505					510											
ctc	atc	tcg	ctg	aca	ttt	ttg	act	gta	act	gat	ctt	att	ggc	ctg	cca	1763				
Leu	Ile	Ser	Leu	Thr	Phe	Leu	Thr	Val	Thr	Asp	Leu	Ile	Gly	Leu	Pro					
515			520					525												
tgg	gtg	tgc	ttt	ata	tat	aca	atc	atg	agt	cta	gca	tcc	ctg	ctt	ttt	1811				
Trp	Val	Cys	Phe	Ile	Tyr	Thr	Ile	Met	Ser	Leu	Ala	Ser	Leu	Leu	Phe					
530			535					540												
gtt	gtt	atg	ttt	ata	cct	gag	aca	aag	gga	tgc	tct	ttg	gaa	caa	ata	1859				
Val	Val	Met	Phe	Ile	Pro	Glu	Thr	Lys	Gly	Cys	Ser	Leu	Glu	Gln	Ile					
545			550					555					560							
tca	atg	gag	cta	gca	aaa	gtg	aac	tat	gtg	aaa	aac	aac	att	tgt	ttt	1907				
Ser	Met	Glu	Leu	Ala	Lys	Val	Asn	Tyr	Val	Lys	Asn	Asn	Ile	Cys	Phe					
565					570					575										
atg	agt	cat	cac	caa	gaa	gaa	tta	gtg	cca	aaa	cag	cct	caa	aaa	aga	1955				
Met	Ser	His	His	Gln	Glu	Glu	Leu	Val	Pro	Lys	Gln	Pro	Gln	Lys	Arg					
580				585					590											

1283
1331
1379
1427
1475
1523
1571
1619
1667
1715
1763
1811
1859
1907
1955

aaa ccc cag gag cag ctc ttg gag tgt aac aag ctg tgt ggt agg ggc 2003
Lys Pro Gln Glu Gln Leu Leu Glu Cys Asn Lys Leu Cys Gly Arg Gly
595 600 605

caa tcc agg cag ctt tct cca gag acc taa tggcctcaac accttctgaa 2053
Gln Ser Arg Gln Leu Ser Pro Glu Thr *
610 615

cgtggatagt gccagaacac ttaggagggt gtctttggac caatgcatag ttgcgactcc 2113
tgtgtctctt ttccagtgtc atggaactgg ttttgaagag acactctgaa atgataaaga 2173
cagcctttta tccccctcct cccagaagg aacctcaaaa ggtagatgag gtacaagggtc 2233
ctaagtgtac tctttttctg agcaggatat cagggttaaaa aaaaaaagtt actggctggt 2293
ttaatacttt ctaccttctt cacagagcag cctttgaata gactatgtcc tagtgaagac 2353
atcaacctcc gccttaagct atgtatgtat ggaggccagt cgcagcttta ttatgcagac 2413
acacaagtgg tctggacatg agggtagagt ttctgcctac caagacacta cttgcactgg 2473
atcttacgca aaaaaagaacc agaacacaca gtgtggacaa ctgcccataat attctatcta 2533
gattaggaga ggttcctggc taggatttta gtgtgaattc ctagttacat tcaacaagta 2593
taaagattat agagcttatt ttatgaacta taaactataa tttaatgcaa aatatccttt 2653
tatgaatttc atgttaatat tgtgaaatat taaaataatt ccgcaataaa aaaaaaaaaa 2713
aagggcggcc gc 2725

<210> 2
<211> 617
<212> PRT
<213> Homo sapiens

<400> 2
Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
1 5 10 15
Gly Thr Ala Val Glu Thr Glu Gly Ser Gly Ser Arg His Pro Pro Trp
20 25 30
Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Thr Ala Ala
35 40 45
Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
50 55 60
Leu Leu Gln Ile Lys Thr Leu Leu Ala Leu Ser Cys His Glu Gln Glu
65 70 75 80
Met Val Val Ser Ser Leu Val Ile Gly Ala Leu Leu Ala Ser Leu Thr
85 90 95
Gly Gly Val Leu Ile Asp Arg Tyr Gly Arg Arg Thr Ala Ile Ile Leu
100 105 110
Ser Ser Cys Leu Leu Gly Leu Gly Ser Leu Val Leu Ile Leu Ser Leu
115 120 125
Ser Tyr Thr Val Leu Ile Val Gly Arg Ile Ala Ile Gly Val Ser Ile
130 135 140
Ser Leu Ser Ser Ile Ala Thr Cys Val Tyr Ile Ala Glu Ile Ala Pro
145 150 155 160
Gln His Arg Arg Gly Leu Leu Val Ser Leu Asn Glu Leu Met Ile Val
165 170 175
Ile Gly Ile Leu Ser Ala Tyr Ile Ser Asn Tyr Ala Phe Ala Asn Val
180 185 190
Phe His Gly Trp Lys Tyr Met Phe Gly Leu Val Ile Pro Leu Gly Val
195 200 205
Leu Gln Ala Ile Ala Met Tyr Phe Leu Pro Pro Ser Pro Arg Phe Leu
210 215 220
Val Met Lys Gly Gln Glu Gly Ala Ala Ser Lys Val Leu Gly Arg Leu
225 230 235 240
Arg Ala Leu Ser Asp Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser
245 250 255
Leu Lys Asp Glu Tyr Gln Tyr Ser Phe Trp Asp Leu Phe Arg Ser Lys

40045213404


```

      260      265      270
Asp Asn Met Arg Thr Arg Ile Met Ile Gly Leu Thr Leu Val Phe Phe
      275      280      285
Val Gln Ile Thr Gly Gln Pro Asn Ile Leu Phe Tyr Ala Ser Thr Val
      290      295      300
Leu Lys Ser Val Gly Phe Gln Ser Asn Glu Ala Ala Ser Leu Ala Ser
305      310      315      320
Thr Gly Val Gly Val Val Lys Val Ile Ser Thr Ile Pro Ala Thr Leu
      325      330      335
Leu Val Asp His Val Gly Ser Lys Thr Phe Leu Cys Ile Gly Ser Ser
      340      345      350
Val Met Ala Ala Ser Leu Val Thr Met Gly Ile Val Asn Leu Asn Ile
      355      360      365
His Met Asn Phe Thr His Ile Cys Arg Ser His Asn Ser Ile Asn Gln
      370      375      380
Ser Leu Asp Glu Ser Val Ile Tyr Gly Pro Gly Asn Leu Ser Thr Asn
385      390      395      400
Asn Asn Thr Leu Arg Asp His Phe Lys Gly Ile Ser Ser His Ser Arg
      405      410      415
Ser Ser Leu Met Pro Leu Arg Asn Asp Val Asp Lys Arg Gly Glu Thr
      420      425      430
Thr Ser Ala Ser Leu Leu Asn Ala Gly Leu Ser His Thr Glu Tyr Gln
      435      440      445
Ile Val Thr Asp Pro Gly Asp Val Pro Ala Phe Leu Lys Trp Leu Ser
      450      455      460
Leu Ala Ser Leu Leu Val Tyr Val Ala Ala Phe Ser Ile Gly Leu Gly
465      470      475      480
Pro Met Pro Trp Leu Val Leu Ser Glu Ile Phe Pro Gly Gly Ile Arg
      485      490      495
Gly Arg Ala Met Ala Leu Thr Ser Ser Met Asn Trp Gly Ile Asn Leu
      500      505      510
Leu Ile Ser Leu Thr Phe Leu Thr Val Thr Asp Leu Ile Gly Leu Pro
      515      520      525
Trp Val Cys Phe Ile Tyr Thr Ile Met Ser Leu Ala Ser Leu Leu Phe
      530      535      540
Val Val Met Phe Ile Pro Glu Thr Lys Gly Cys Ser Leu Glu Gln Ile
545      550      555      560
Ser Met Glu Leu Ala Lys Val Asn Tyr Val Lys Asn Asn Ile Cys Phe
      565      570      575
Met Ser His His Gln Glu Glu Leu Val Pro Lys Gln Pro Gln Lys Arg
      580      585      590
Lys Pro Gln Glu Gln Leu Leu Glu Cys Asn Lys Leu Cys Gly Arg Gly
      595      600      605
Gln Ser Arg Gln Leu Ser Pro Glu Thr
      610      615

```

<210> 3
 <211> 1854
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1854)

```

<400> 3
atg gta cct gtt gaa aac acc gag ggc ccc agt ctg ctg aac cag aag
Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
  1             5             10             15

```


500 505 510

ctc atc tcg ctg aca ttt ttg act gta act gat ctt att ggc ctg cca 1584
 Leu Ile Ser Leu Thr Phe Leu Thr Val Thr Asp Leu Ile Gly Leu Pro
 515 520 525

tgg gtg tgc ttt ata tat aca atc atg agt cta gca tcc ctg ctt ttt 1632
 Trp Val Cys Phe Ile Tyr Thr Ile Met Ser Leu Ala Ser Leu Leu Phe
 530 535 540

gtt gtt atg ttt ata cct gag aca aag gga tgc tct ttg gaa caa ata 1680
 Val Val Met Phe Ile Pro Glu Thr Lys Gly Cys Ser Leu Glu Gln Ile
 545 550 555 560

tca atg gag cta gca aaa gtg aac tat gtg aaa aac aac att tgt ttt 1728
 Ser Met Glu Leu Ala Lys Val Asn Tyr Val Lys Asn Asn Ile Cys Phe
 565 570 575

atg agt cat cac caa gaa gaa tta gtg cca aaa cag cct caa aaa aga 1776
 Met Ser His His Gln Glu Glu Leu Val Pro Lys Gln Pro Gln Lys Arg
 580 585 590

aaa ccc cag gag cag ctc ttg gag tgt aac aag ctg tgt ggt agg ggc 1824
 Lys Pro Gln Glu Gln Leu Leu Glu Cys Asn Lys Leu Cys Gly Arg Gly
 595 600 605

caa tcc agg cag ctt tct cca gag acc taa 1854
 Gln Ser Arg Gln Leu Ser Pro Glu Thr *
 610 615

<210> 4
 <211> 2230
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (376)...(1962)

<400> 4
 gtcgacccac gcgtccggca acatggcggc tgccgtggtg cagcgcccg gctgagcgac 60
 agcaagtga gcggtctcct acccgggtg aggggtggc tccgctggg atcgtgccct 120
 ctccagcccg ctctgtccc cgacatcacg tgtattccg acgtccctc cgcgtgtgt 180
 gtctactgag acggggaggc gtgacaggc ccgggtccct tctcagtgt gctctgtgt 240
 tcagggaag ctcccgtct ccgggcgcac ttccctcgcc tgtgttcggg ccatcctcct 300
 ttctccagcc tctccctc gcaggtggga tcgtcgggtg gaccggagcg cgggcgggcg 360
 cggcccccg ggacc atg gcc ggg tcc gac acc gcg ccc ttc ctc agc cag 411
 Met Ala Gly Ser Asp Thr Ala Pro Phe Leu Ser Gln
 1 5 10

gcg gat gac ccg gac gac ggg cca gtg cct ggc acc ccg ggg ttg cca 459
 Ala Asp Asp Pro Asp Asp Gly Pro Val Pro Gly Thr Pro Gly Leu Pro
 15 20 25

ggg tcc acg ggg aac ccg aag tcc gag gag ccc gag gtc ccg gac cag 507
 Gly Ser Thr Gly Asn Pro Lys Ser Glu Glu Pro Glu Val Pro Asp Gln
 30 35 40

gag ggg ctg cag cgc atc acc ggc ctg tct ccc ggc cgt tcg gct ctc 555
 Glu Gly Leu Gln Arg Ile Thr Gly Leu Ser Pro Gly Arg Ser Ala Leu
 45 50 55 60

T0214CP "E294200"

tcc cgc gtg gtc ctt ggg gag acc cca ccc tgc ctt ccc gga gac tcc 1323
 Ser Arg Val Val Leu Gly Glu Thr Pro Pro Cys Leu Pro Gly Asp Ser
 305 310 315

tgc tct tcc tct gac agt ctc atc ttt gga ctc atc acc tgc ctg acc 1371
 Cys Ser Ser Ser Asp Ser Leu Ile Phe Gly Leu Ile Thr Cys Leu Thr
 320 325 330

gga gtc ctg ggt gtg ggc ctg ggt gtg gag atc agc cgc cgg ctc cgc 1419
 Gly Val Leu Gly Val Gly Leu Gly Val Glu Ile Ser Arg Arg Leu Arg
 335 340 345

cac tcc aac ccc cgg gct gat ccc ctg gtc tgt gcc act ggc ctc ctg 1467
 His Ser Asn Pro Arg Ala Asp Pro Leu Val Cys Ala Thr Gly Leu Leu
 350 355 360

ggc tct gca ccc ttc ctc ttc ctg tcc ctt gcc tgc gcc cgt ggt agc 1515
 Gly Ser Ala Pro Phe Leu Phe Leu Ser Leu Ala Cys Ala Arg Gly Ser
 365 370 375 380

atc gtg gcc act tat att ttc atc ttc att gga gag acc ctc ctg tcc 1563
 Ile Val Ala Thr Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu Leu Ser
 385 390 395

atg aac tgg gcc atc gtg gcc gac att ctg ctg tac gtg gtg atc cct 1611
 Met Asn Trp Ala Ile Val Ala Asp Ile Leu Leu Tyr Val Val Ile Pro
 400 405 410

acc cga cgc tcc acc gcc gag gcc ttc cag atc gtg ctg tcc cac ctg 1659
 Thr Arg Arg Ser Thr Ala Glu Ala Phe Gln Ile Val Leu Ser His Leu
 415 420 425

ctg ggt gat gct ggg agc ccc tac ctc att ggc ctg atc tct gac cgc 1707
 Leu Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser Asp Arg
 430 435 440

ctg cgc cgg aac tgg ccc ccc tcc ttc ttg tcc gag ttc cgg gct ctg 1755
 Leu Arg Arg Asn Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg Ala Leu
 445 450 455 460

cag ttc tcg ctc atg ctc tgc gcg ttt gtt ggg gca ctg ggc ggc gca 1803
 Gln Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly Gly Ala
 465 470 475

gcc ttc ctg ggc acc gcc atc ttc att gag gcc gac cgc cgg cgg gca 1851
 Ala Phe Leu Gly Thr Ala Ile Phe Ile Glu Ala Asp Arg Arg Arg Ala
 480 485 490

cag ctg cac gtg cag ggc ctg ctg cac gaa gca ggg tcc aca gac gac 1899
 Gln Leu His Val Gln Gly Leu Leu His Glu Ala Gly Ser Thr Asp Asp
 495 500 505

cgg att gtg gtg ccc cag cgg ggc cgc tcc acc cgc gtg ccc gtg gcc 1947
 Arg Ile Val Val Pro Gln Arg Gly Arg Ser Thr Arg Val Pro Val Ala
 510 515 520

agt gtg ctc atc tga gaggtgccg ctcacctacc tgcacatctg ccacagctgg 2002
 Ser Val Leu Ile *
 525

ccctgggccc accccacgaa gggcctgggc ctaaccctt ggcttgcccc agcttcaga 2062

T02T "E23420T"

				405					410					415			
Thr	Ala	Glu	Ala	Phe	Gln	Ile	Val	Leu	Ser	His	Leu	Leu	Gly	Asp	Ala		
			420					425					430				
Gly	Ser	Pro	Tyr	Leu	Ile	Gly	Leu	Ile	Ser	Asp	Arg	Leu	Arg	Arg	Asn		
		435					440					445					
Trp	Pro	Pro	Ser	Phe	Leu	Ser	Glu	Phe	Arg	Ala	Leu	Gln	Phe	Ser	Leu		
	450					455					460						
Met	Leu	Cys	Ala	Phe	Val	Gly	Ala	Leu	Gly	Gly	Ala	Ala	Phe	Leu	Gly		
465					470				475						480		
Thr	Ala	Ile	Phe	Ile	Glu	Ala	Asp	Arg	Arg	Arg	Ala	Gln	Leu	His	Val		
			485					490					495				
Gln	Gly	Leu	Leu	His	Glu	Ala	Gly	Ser	Thr	Asp	Asp	Arg	Ile	Val	Val		
		500						505					510				
Pro	Gln	Arg	Gly	Arg	Ser	Thr	Arg	Val	Pro	Val	Ala	Ser	Val	Leu	Ile		
	515						520					525					

<210> 6
 <211> 1587
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1587)

<400> 6																
atg	gcc	ggg	tcc	gac	acc	gcg	ccc	ttc	ctc	agc	cag	gcg	gat	gac	ccg	48
Met	Ala	Gly	Ser	Asp	Thr	Ala	Pro	Phe	Leu	Ser	Gln	Ala	Asp	Asp	Pro	
1				5				10					15			
gac gac ggg cca gtg cct ggc acc ccg ggg ttg cca ggg tcc acg ggg																96
Asp	Asp	Gly	Pro	Val	Pro	Gly	Thr	Pro	Gly	Leu	Pro	Gly	Ser	Thr	Gly	
			20					25					30			
aac ccg aag tcc gag gag ccc gag gtc ccg gac cag gag ggg ctg cag																144
Asn	Pro	Lys	Ser	Glu	Glu	Pro	Glu	Val	Pro	Asp	Gln	Glu	Gly	Leu	Gln	
		35					40					45				
cgc atc acc ggc ctg tct ccc ggc cgt tcg gct ctc ata gtg gcg gtg																192
Arg	Ile	Thr	Gly	Leu	Ser	Pro	Gly	Arg	Ser	Ala	Leu	Ile	Val	Ala	Val	
	50					55					60					
ctg tgc tac atc aat ctc ctg aac tac atg gac cgc ttc acc gtg gct																240
Leu	Cys	Tyr	Ile	Asn	Leu	Leu	Asn	Tyr	Met	Asp	Arg	Phe	Thr	Val	Ala	
65				70				75					80			
ggc gtc ctt ccc gac atc gag cag ttc ttc aac atc ggg gac agt agc																288
Gly	Val	Leu	Pro	Asp	Ile	Glu	Gln	Phe	Phe	Asn	Ile	Gly	Asp	Ser	Ser	
			85					90					95			
tct ggg ctc atc cag acc gtg ttc atc tcc agt tac atg gtg ttg gca																336
Ser	Gly	Leu	Ile	Gln	Thr	Val	Phe	Ile	Ser	Ser	Tyr	Met	Val	Leu	Ala	
			100				105						110			
cct gtg ttt ggc tac ctg ggt gac agg tac aat cgg aag tat ctc atg																384
Pro	Val	Phe	Gly	Tyr	Leu	Gly	Asp	Arg	Tyr	Asn	Arg	Lys	Tyr	Leu	Met	
		115					120					125				
tgc ggg ggc att gcc ttc tgg tcc ctg gtg aca ctg ggg tca tcc ttc																432
Cys	Gly	Gly	Ile	Ala	Phe	Trp	Ser	Leu	Val	Thr	Leu	Gly	Ser	Ser	Phe	

The "Sequence" file

tat att ttc atc ttc att gga gag acc ctc ctg tcc atg aac tgg gcc 1200
 Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala
 385 390 395 400

 atc gtg gcc gac att ctg ctg tac gtg gtg atc cct acc cga cgc tcc 1248
 Ile Val Ala Asp Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser
 405 410 415

 acc gcc gag gcc ttc cag atc gtg ctg tcc cac ctg ctg ggt gat gct 1296
 Thr Ala Glu Ala Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala
 420 425 430

 ggg agc ccc tac ctc att ggc ctg atc tct gac cgc ctg cgc cgg aac 1344
 Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn
 435 440 445

 tgg ccc ccc tcc ttc ttg tcc gag ttc cgg gct ctg cag ttc tcg ctc 1392
 Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu
 450 455 460

 atg ctc tgc gcg ttt gtt ggg gca ctg ggc ggc gca gcc ttc ctg ggc 1440
 Met Leu Cys Ala Phe Val Gly Ala Leu Gly Gly Ala Ala Phe Leu Gly
 465 470 475 480

 acc gcc atc ttc att gag gcc gac cgc cgg cgg gca cag ctg cac gtg 1488
 Thr Ala Ile Phe Ile Glu Ala Asp Arg Arg Arg Ala Gln Leu His Val
 485 490 495

 cag ggc ctg ctg cac gaa gca ggg tcc aca gac gac cgg att gtg gtg 1536
 Gln Gly Leu Leu His Glu Ala Gly Ser Thr Asp Asp Arg Ile Val Val
 500 505 510

 ccc cag cgg ggc cgc tcc acc cgc gtg ccc gtg gcc agt gtg ctc atc 1584
 Pro Gln Arg Gly Arg Ser Thr Arg Val Pro Val Ala Ser Val Leu Ile
 515 520 525

 tga 1587
 *

<210> 7
 <211> 4632
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (225)...(3581)

<220>
 <221> misc_feature
 <222> (4611)
 <223> n = a,c,t, or g

<400> 7
 cacgcgtccg cccacgcgtc cgcccacgcg tccgagcccc ctttcaagcc ttagcttccg 60
 gctccaagcc gacccctcc ccctccctgt ccccttcccc ttctcccatc cctctctcgg 120
 ccacagcgtc ttgttagtcc tctccctcta ctcgcaata tttctttct ttctccctcc 180
 tctctcccat ttgttgtttg atgtttccca ctctttgagg aagg atg gtt gat ttg 236
 Met Val Asp Leu

gag agc gaa gtg ccc cct ctg cct ccc agg tac agg ttt cga gat ttg 284
 Glu Ser Glu Val Pro Pro Leu Pro Pro Arg Tyr Arg Phe Arg Asp Leu
 5 10 15 20
 ctg cta ggg gac caa gga tgg caa aac gat gac aga gta caa gtt gaa 332
 Leu Leu Gly Asp Gln Gly Trp Gln Asn Asp Asp Arg Val Gln Val Glu
 25 30 35
 ttc tat atg aat gaa aat aca ttt aaa gaa aga cta aaa tta ttt ttc 380
 Phe Tyr Met Asn Glu Asn Thr Phe Lys Glu Arg Leu Lys Leu Phe Phe
 40 45 50
 ata aaa aac cag aga tca agt cta agg ata cgc ctg ttc aat ttt tct 428
 Ile Lys Asn Gln Arg Ser Ser Leu Arg Ile Arg Leu Phe Asn Phe Ser
 55 60 65
 ctc aaa tta cta agc tgc tta tta tac ata atc cga gta cta cta gaa 476
 Leu Lys Leu Leu Ser Cys Leu Leu Tyr Ile Ile Arg Val Leu Leu Glu
 70 75 80
 aac cct tca caa gga aat gaa tgg tct cat atc ttt tgg gtg aac aga 524
 Asn Pro Ser Gln Gly Asn Glu Trp Ser His Ile Phe Trp Val Asn Arg
 85 90 95 100
 agt cta cct ttg tgg ggc tta cag gtt tca gtg gca ttg ata agt ctg 572
 Ser Leu Pro Leu Trp Gly Leu Gln Val Ser Val Ala Leu Ile Ser Leu
 105 110 115
 ttt gaa aca ata tta ctt ggt tat ctt agt tat aag gga aac atc tgg 620
 Phe Glu Thr Ile Leu Leu Gly Tyr Leu Ser Tyr Lys Gly Asn Ile Trp
 120 125 130
 gaa cag att tta cga ata ccc ttc atc ttg gaa ata att aat gca gtt 668
 Glu Gln Ile Leu Arg Ile Pro Phe Ile Leu Glu Ile Ile Asn Ala Val
 135 140 145
 ccc ttc att atc tca ata ttc tgg cct tcc tta agg aat cta ttt gtc 716
 Pro Phe Ile Ile Ser Ile Phe Trp Pro Ser Leu Arg Asn Leu Phe Val
 150 155 160
 cca gtc ttt ctg aac tgt tgg ctt gcc aaa cat gcc ttg gaa aat atg 764
 Pro Val Phe Leu Asn Cys Trp Leu Ala Lys His Ala Leu Glu Asn Met
 165 170 175 180
 att aat gat cta cac aga gcc att cag cgt aca cag tct gca atg ttt 812
 Ile Asn Asp Leu His Arg Ala Ile Gln Arg Thr Gln Ser Ala Met Phe
 185 190 195
 aat caa gtt ttg att tta ata tct aca tta cta tgc ctt atc ttc acc 860
 Asn Gln Val Leu Ile Leu Ile Ser Thr Leu Leu Cys Leu Ile Phe Thr
 200 205 210
 tgc att tgt ggg atc caa cat ctg gaa cga ata gga aag agg ctg aat 908
 Cys Ile Cys Gly Ile Gln His Leu Glu Arg Ile Gly Lys Arg Leu Asn
 215 220 225
 ctc ttt gac tcc ctt tat ttc tgc att gtg acg ttt tct act gtg ggc 956
 Leu Phe Asp Ser Leu Tyr Phe Cys Ile Val Thr Phe Ser Thr Val Gly
 230 235 240

100445
 62342007

ttc ggg gat gtc act cct gaa aca tgg tcc tcc aag ctt ttt gta gtt 1004
 Phe Gly Asp Val Thr Pro Glu Thr Trp Ser Ser Lys Leu Phe Val Val
 245 250 255 260

gct atg att tgt gtt gct ctt gtg gtt cta ccc ata cag ttt gaa cag 1052
 Ala Met Ile Cys Val Ala Leu Val Val Leu Pro Ile Gln Phe Glu Gln
 265 270 275

ctg gct tat ttg tgg atg gag aga caa aag tca gga gga aac tat agt 1100
 Leu Ala Tyr Leu Trp Met Glu Arg Gln Lys Ser Gly Gly Asn Tyr Ser
 280 285 290

cga cat aga gct caa act gaa aag cat gtc gtc ctg tgt gtc agc tca 1148
 Arg His Arg Ala Gln Thr Glu Lys His Val Val Leu Cys Val Ser Ser
 295 300 305

ctg aag att gat tta ctt atg gat ttt tta aat gaa ttc tat gct cat 1196
 Leu Lys Ile Asp Leu Leu Met Asp Phe Leu Asn Glu Phe Tyr Ala His
 310 315 320

cct agg ctc cag gat tat tat gtg gtg att ttg tgt cct act gaa atg 1244
 Pro Arg Leu Gln Asp Tyr Tyr Val Val Ile Leu Cys Pro Thr Glu Met
 325 330 335 340

gat gta cag gtt cga agg gta ctg cag att cca atg tgg tcc caa cga 1292
 Asp Val Gln Val Arg Arg Val Leu Gln Ile Pro Met Trp Ser Gln Arg
 345 350 355

gtt atc tac ctt caa ggt tca gcc ctt aaa gat caa gac cta ttg aga 1340
 Val Ile Tyr Leu Gln Gly Ser Ala Leu Lys Asp Gln Asp Leu Leu Arg
 360 365 370

gca aag atg gat gac gct gag gcc tgt ttt att ctc agt agc cgt tgt 1388
 Ala Lys Met Asp Asp Ala Glu Ala Cys Phe Ile Leu Ser Ser Arg Cys
 375 380 385

gaa gtg gat agg aca tca tct gat cac caa aca att ttg aga gca tgg 1436
 Glu Val Asp Arg Thr Ser Ser Asp His Gln Thr Ile Leu Arg Ala Trp
 390 395 400

gct gtg aaa gat ttt gct cca aat tgt cct ttg tat gtc cag ata tta 1484
 Ala Val Lys Asp Phe Ala Pro Asn Cys Pro Leu Tyr Val Gln Ile Leu
 405 410 415 420

aag cct gaa aat aaa ttt cac atc aaa ttt gct gat cat gtt gtt tgt 1532
 Lys Pro Glu Asn Lys Phe His Ile Lys Phe Ala Asp His Val Val Cys
 425 430 435

gaa gaa gag ttt aaa tac gcc atg tta gct tta aac tgt ata tgc cca 1580
 Glu Glu Glu Phe Lys Tyr Ala Met Leu Ala Leu Asn Cys Ile Cys Pro
 440 445 450

gca aca tct aca ctt att aca cta ctg gtt cat acc tct aga ggg caa 1628
 Ala Thr Ser Thr Leu Ile Thr Leu Leu Val His Thr Ser Arg Gly Gln
 455 460 465

gaa ggc cag caa tcg cca gaa caa tgg cag aag atg tac ggt aga tgc 1676
 Glu Gly Gln Gln Ser Pro Glu Gln Trp Gln Lys Met Tyr Gly Arg Cys
 470 475 480

tcc ggg aat gaa gtc tac cac att gtt ttg gaa gaa agt aca ttt ttt 1724

1004
 1052
 1100
 1148
 1196
 1244
 1292
 1340
 1388
 1436
 1484
 1532
 1580
 1628
 1676
 1724

Ser Gly Asn Glu Val Tyr His Ile Val Leu Glu Glu Ser Thr Phe Phe
 485 490 495 500

 gct gaa tat gaa gga aag agt ttt aca tat gcc tct ttc cat gca cac 1772
 Ala Glu Tyr Glu Gly Lys Ser Phe Thr Tyr Ala Ser Phe His Ala His
 505 510 515

 aaa aag ttt ggc gtc tgc ttg att ggt gtt agg agg gag gat aat aaa 1820
 Lys Lys Phe Gly Val Cys Leu Ile Gly Val Arg Arg Glu Asp Asn Lys
 520 525 530

 aac att ttg ctg aat cca ggt cct cga tac att atg aat tct acg gac 1868
 Asn Ile Leu Leu Asn Pro Gly Pro Arg Tyr Ile Met Asn Ser Thr Asp
 535 540 545

 ata tgc ttt tat att aat att acc aaa gaa gag aat tca gca ttt aaa 1916
 Ile Cys Phe Tyr Ile Asn Ile Thr Lys Glu Glu Asn Ser Ala Phe Lys
 550 555 560

 aac caa gac cag cag aga aaa agc aat gtg tcc agg tcg ttt tat cat 1964
 Asn Gln Asp Gln Gln Arg Lys Ser Asn Val Ser Arg Ser Phe Tyr His
 565 570 575 580

 gga cct tcc aga tta cct gta cat agc ata att gcc agc atg ggt act 2012
 Gly Pro Ser Arg Leu Pro Val His Ser Ile Ile Ala Ser Met Gly Thr
 585 590 595

 gtg gct ata gac ctg caa gat aca agc tgt aga tca gca agt ggc cct 2060
 Val Ala Ile Asp Leu Gln Asp Thr Ser Cys Arg Ser Ala Ser Gly Pro
 600 605 610

 acc ctg tct ctt cct aca gag gga agc aaa gaa ata aga aga cct agc 2108
 Thr Leu Ser Leu Pro Thr Glu Gly Ser Lys Glu Ile Arg Arg Pro Ser
 615 620 625

 att gct cct gtt tta gag gtt gca gat aca tca tcg att caa aca tgt 2156
 Ile Ala Pro Val Leu Glu Val Ala Asp Thr Ser Ser Ile Gln Thr Cys
 630 635 640

 gat ctt cta agt gac caa tca gaa gat gaa act aca cca gat gaa gaa 2204
 Asp Leu Leu Ser Asp Gln Ser Glu Asp Glu Thr Thr Pro Asp Glu Glu
 645 650 655 660

 atg tct tca aac tta gag tat gct aaa ggt tac cca cct tat tct cca 2252
 Met Ser Ser Asn Leu Glu Tyr Ala Lys Gly Tyr Pro Pro Tyr Ser Pro
 665 670 675

 tat ata gga agt tca ccc act ttt tgt cat ctc ctt cat gaa aaa gta 2300
 Tyr Ile Gly Ser Ser Pro Thr Phe Cys His Leu Leu His Glu Lys Val
 680 685 690

 cca ttt tgc tgc tta aga tta gac aag agt tgc caa cat aac tac tat 2348
 Pro Phe Cys Cys Leu Arg Leu Asp Lys Ser Cys Gln His Asn Tyr Tyr
 695 700 705

 gag gat gca aaa gcc tat gga ttc aaa aat aaa cta att ata gtt gca 2396
 Glu Asp Ala Lys Ala Tyr Gly Phe Lys Asn Lys Leu Ile Ile Val Ala
 710 715 720

 gct gaa aca gct gga aat gga tta tat aac ttt att gtt cct ctc agg 2444
 Ala Glu Thr Ala Gly Asn Gly Leu Tyr Asn Phe Ile Val Pro Leu Arg

100463 "E254200T"

<400> 8

Met	Val	Asp	Leu	Glu	Ser	Glu	Val	Pro	Pro	Leu	Pro	Pro	Arg	Tyr	Arg
1				5					10					15	
Phe	Arg	Asp	Leu	Leu	Leu	Gly	Asp	Gln	Gly	Trp	Gln	Asn	Asp	Asp	Arg
			20					25					30		
Val	Gln	Val	Glu	Phe	Tyr	Met	Asn	Glu	Asn	Thr	Phe	Lys	Glu	Arg	Leu
		35					40					45			
Lys	Leu	Phe	Phe	Ile	Lys	Asn	Gln	Arg	Ser	Ser	Leu	Arg	Ile	Arg	Leu
	50				55					60					
Phe	Asn	Phe	Ser	Leu	Lys	Leu	Leu	Ser	Cys	Leu	Leu	Tyr	Ile	Ile	Arg
65					70					75				80	
Val	Leu	Leu	Glu	Asn	Pro	Ser	Gln	Gly	Asn	Glu	Trp	Ser	His	Ile	Phe
				85					90					95	
Trp	Val	Asn	Arg	Ser	Leu	Pro	Leu	Trp	Gly	Leu	Gln	Val	Ser	Val	Ala
			100					105					110		
Leu	Ile	Ser	Leu	Phe	Glu	Thr	Ile	Leu	Leu	Gly	Tyr	Leu	Ser	Tyr	Lys
		115					120					125			
Gly	Asn	Ile	Trp	Glu	Gln	Ile	Leu	Arg	Ile	Pro	Phe	Ile	Leu	Glu	Ile
	130					135					140				
Ile	Asn	Ala	Val	Pro	Phe	Ile	Ile	Ser	Ile	Phe	Trp	Pro	Ser	Leu	Arg
145					150					155					160
Asn	Leu	Phe	Val	Pro	Val	Phe	Leu	Asn	Cys	Trp	Leu	Ala	Lys	His	Ala
			165						170					175	
Leu	Glu	Asn	Met	Ile	Asn	Asp	Leu	His	Arg	Ala	Ile	Gln	Arg	Thr	Gln
		180					185						190		
Ser	Ala	Met	Phe	Asn	Gln	Val	Leu	Ile	Leu	Ile	Ser	Thr	Leu	Leu	Cys
	195						200					205			
Leu	Ile	Phe	Thr	Cys	Ile	Cys	Gly	Ile	Gln	His	Leu	Glu	Arg	Ile	Gly
	210				215						220				
Lys	Arg	Leu	Asn	Leu	Phe	Asp	Ser	Leu	Tyr	Phe	Cys	Ile	Val	Thr	Phe
225					230					235					240
Ser	Thr	Val	Gly	Phe	Gly	Asp	Val	Thr	Pro	Glu	Thr	Trp	Ser	Ser	Lys
			245						250					255	
Leu	Phe	Val	Val	Ala	Met	Ile	Cys	Val	Ala	Leu	Val	Val	Leu	Pro	Ile
		260						265					270		
Gln	Phe	Glu	Gln	Leu	Ala	Tyr	Leu	Trp	Met	Glu	Arg	Gln	Lys	Ser	Gly
		275					280					285			
Gly	Asn	Tyr	Ser	Arg	His	Arg	Ala	Gln	Thr	Glu	Lys	His	Val	Val	Leu
	290					295					300				
Cys	Val	Ser	Ser	Leu	Lys	Ile	Asp	Leu	Leu	Met	Asp	Phe	Leu	Asn	Glu
305					310					315					320
Phe	Tyr	Ala	His	Pro	Arg	Leu	Gln	Asp	Tyr	Tyr	Val	Val	Ile	Leu	Cys
			325						330					335	
Pro	Thr	Glu	Met	Asp	Val	Gln	Val	Arg	Arg	Val	Leu	Gln	Ile	Pro	Met
		340						345					350		
Trp	Ser	Gln	Arg	Val	Ile	Tyr	Leu	Gln	Gly	Ser	Ala	Leu	Lys	Asp	Gln
		355					360					365			
Asp	Leu	Leu	Arg	Ala	Lys	Met	Asp	Asp	Ala	Glu	Ala	Cys	Phe	Ile	Leu
	370					375					380				
Ser	Ser	Arg	Cys	Glu	Val	Asp	Arg	Thr	Ser	Ser	Asp	His	Gln	Thr	Ile
385					390					395					400
Leu	Arg	Ala	Trp	Ala	Val	Lys	Asp	Phe	Ala	Pro	Asn	Cys	Pro	Leu	Tyr
			405						410					415	
Val	Gln	Ile	Leu	Lys	Pro	Glu	Asn	Lys	Phe	His	Ile	Lys	Phe	Ala	Asp
		420						425					430		
His	Val	Val	Cys	Glu	Glu	Glu	Phe	Lys	Tyr	Ala	Met	Leu	Ala	Leu	Asn
		435					440					445			
Cys	Ile	Cys	Pro	Ala	Thr	Ser	Thr	Leu	Ile	Thr	Leu	Leu	Val	His	Thr
	450					455					460				
Ser	Arg	Gly	Gln	Glu	Gly	Gln	Gln	Ser	Pro	Glu	Gln	Trp	Gln	Lys	Met
465					470					475					480

T.C.T. 400433 400433

Tyr Gly Arg Cys Ser Gly Asn Glu Val Tyr His Ile Val Leu Glu Glu
 485 490 495
 Ser Thr Phe Phe Ala Glu Tyr Glu Gly Lys Ser Phe Thr Tyr Ala Ser
 500 505 510
 Phe His Ala His Lys Lys Phe Gly Val Cys Leu Ile Gly Val Arg Arg
 515 520 525
 Glu Asp Asn Lys Asn Ile Leu Leu Asn Pro Gly Pro Arg Tyr Ile Met
 530 535 540
 Asn Ser Thr Asp Ile Cys Phe Tyr Ile Asn Ile Thr Lys Glu Glu Asn
 545 550 555 560
 Ser Ala Phe Lys Asn Gln Asp Gln Gln Arg Lys Ser Asn Val Ser Arg
 565 570 575
 Ser Phe Tyr His Gly Pro Ser Arg Leu Pro Val His Ser Ile Ile Ala
 580 585 590
 Ser Met Gly Thr Val Ala Ile Asp Leu Gln Asp Thr Ser Cys Arg Ser
 595 600 605
 Ala Ser Gly Pro Thr Leu Ser Leu Pro Thr Glu Gly Ser Lys Glu Ile
 610 615 620
 Arg Arg Pro Ser Ile Ala Pro Val Leu Glu Val Ala Asp Thr Ser Ser
 625 630 635 640
 Ile Gln Thr Cys Asp Leu Leu Ser Asp Gln Ser Glu Asp Glu Thr Thr
 645 650 655
 Pro Asp Glu Glu Met Ser Ser Asn Leu Glu Tyr Ala Lys Gly Tyr Pro
 660 665 670
 Pro Tyr Ser Pro Tyr Ile Gly Ser Ser Pro Thr Phe Cys His Leu Leu
 675 680 685
 His Glu Lys Val Pro Phe Cys Cys Leu Arg Leu Asp Lys Ser Cys Gln
 690 695 700
 His Asn Tyr Tyr Glu Asp Ala Lys Ala Tyr Gly Phe Lys Asn Lys Leu
 705 710 715 720
 Ile Ile Val Ala Ala Glu Thr Ala Gly Asn Gly Leu Tyr Asn Phe Ile
 725 730 735
 Val Pro Leu Arg Ala Tyr Tyr Arg Pro Lys Lys Glu Leu Asn Pro Ile
 740 745 750
 Val Leu Leu Leu Asp Asn Pro Leu Asp Asp Leu Leu Arg Cys Gly Val
 755 760 765
 Thr Phe Ala Ala Asn Met Val Val Val Asp Lys Glu Ser Thr Met Ser
 770 775 780
 Ala Glu Glu Asp Tyr Met Ala Asp Ala Lys Thr Ile Val Asn Val Gln
 785 790 795 800
 Thr Leu Phe Arg Leu Phe Ser Ser Leu Ser Ile Ile Thr Glu Leu Thr
 805 810 815
 His Pro Ala Asn Met Arg Phe Met Gln Phe Arg Ala Lys Asp Cys Tyr
 820 825 830
 Ser Leu Ala Leu Ser Lys Leu Glu Lys Lys Glu Arg Glu Arg Gly Ser
 835 840 845
 Asn Leu Ala Phe Met Phe Arg Leu Pro Phe Ala Ala Gly Arg Val Phe
 850 855 860
 Ser Ile Ser Met Leu Asp Thr Leu Leu Tyr Gln Ser Phe Val Lys Asp
 865 870 875 880
 Tyr Met Ile Ser Ile Thr Arg Leu Leu Leu Gly Leu Asp Thr Thr Pro
 885 890 895
 Gly Ser Gly Phe Leu Cys Ser Met Lys Ile Thr Ala Asp Asp Leu Trp
 900 905 910
 Ile Arg Thr Tyr Ala Arg Leu Tyr Gln Lys Leu Cys Ser Ser Thr Gly
 915 920 925
 Asp Val Pro Ile Gly Ile Tyr Arg Thr Glu Ser Gln Lys Leu Thr Thr
 930 935 940
 Ser Glu Ser Arg Lys Ile Ala Ser Gln Ser Gln Ile Ser Ile Ser Val
 945 950 955 960
 Glu Glu Trp Glu Asp Thr Lys Asp Ser Lys Glu Gln Gly His His Arg

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

```

          965          970          975
Ser Asn His Arg Asn Ser Thr Ser Ser Asp Gln Ser Asp His Pro Leu
          980          985          990
Leu Arg Arg Lys Ser Met Gln Trp Ala Arg Arg Leu Ser Arg Lys Gly
          995          1000          1005
Pro Lys His Ser Gly Lys Thr Ala Glu Lys Ile Thr Gln Gln Arg Leu
          1010          1015          1020
Asn Leu Tyr Arg Arg Ser Glu Arg Gln Glu Leu Ala Glu Leu Val Lys
          1025          1030          1035          1040
Asn Arg Met Lys His Leu Gly Leu Ser Thr Val Gly Tyr Asp Glu Met
          1045          1050          1055
Asn Asp His Gln Ser Thr Leu Ser Tyr Ile Leu Ile Asn Pro Ser Pro
          1060          1065          1070
Asp Thr Arg Ile Glu Leu Asn Asp Val Val Tyr Leu Ile Arg Pro Asp
          1075          1080          1085
Pro Leu Ala Tyr Leu Pro Asn Ser Glu Pro Ser Arg Arg Asn Ser Ile
          1090          1095          1100
Cys Asn Val Thr Gly Gln Asp Ser Arg Glu Glu Thr Gln Leu
          1105          1110          1115

```

```

<210> 9
<211> 3357
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)...(3357)

```

```

<400> 9
atg gtt gat ttg gag agc gaa gtg ccc cct ctg cct ccc agg tac agg 48
Met Val Asp Leu Glu Ser Glu Val Pro Pro Leu Pro Pro Arg Tyr Arg
  1          5          10          15

ttt cga gat ttg ctg cta ggg gac caa gga tgg caa aac gat gac aga 96
Phe Arg Asp Leu Leu Leu Gly Asp Gln Gly Trp Gln Asn Asp Asp Arg
          20          25          30

gta caa gtt gaa ttc tat atg aat gaa aat aca ttt aaa gaa aga cta 144
Val Gln Val Glu Phe Tyr Met Asn Glu Asn Thr Phe Lys Glu Arg Leu
          35          40          45

aaa tta ttt ttc ata aaa aac cag aga tca agt cta agg ata cgc ctg 192
Lys Leu Phe Phe Ile Lys Asn Gln Arg Ser Ser Leu Arg Ile Arg Leu
          50          55          60

ttc aat ttt tct ctc aaa tta cta agc tgc tta tta tac ata atc cga 240
Phe Asn Phe Ser Leu Lys Leu Leu Ser Cys Leu Leu Tyr Ile Ile Arg
          65          70          75          80

gta cta cta gaa aac cct tca caa gga aat gaa tgg tct cat atc ttt 288
Val Leu Leu Glu Asn Pro Ser Gln Gly Asn Glu Trp Ser His Ile Phe
          85          90          95

tgg gtg aac aga agt cta cct ttg tgg ggc tta cag gtt tca gtg gca 336
Trp Val Asn Arg Ser Leu Pro Leu Trp Gly Leu Gln Val Ser Val Ala
          100          105          110

ttg ata agt ctg ttt gaa aca ata tta ctt ggt tat ctt agt tat aag 384
Leu Ile Ser Leu Phe Glu Thr Ile Leu Leu Gly Tyr Leu Ser Tyr Lys

```

The sequence is a DNA sequence.

gca agt ggc cct acc ctg tct ctt cct aca gag gga agc aaa gaa ata	1872
Ala Ser Gly Pro Thr Leu Ser Leu Pro Thr Glu Gly Ser Lys Glu Ile	
610 615 620	
aga aga cct agc att gct cct gtt tta gag gtt gca gat aca tca tcg	1920
Arg Arg Pro Ser Ile Ala Pro Val Leu Glu Val Ala Asp Thr Ser Ser	
625 630 635 640	
att caa aca tgt gat ctt cta agt gac caa tca gaa gat gaa act aca	1968
Ile Gln Thr Cys Asp Leu Leu Ser Asp Gln Ser Glu Asp Glu Thr Thr	
645 650 655	
cca gat gaa gaa atg tct tca aac tta gag tat gct aaa ggt tac cca	2016
Pro Asp Glu Glu Met Ser Ser Asn Leu Glu Tyr Ala Lys Gly Tyr Pro	
660 665 670	
cct tat tct cca tat ata gga agt tca ccc act ttt tgt cat ctc ctt	2064
Pro Tyr Ser Pro Tyr Ile Gly Ser Ser Pro Thr Phe Cys His Leu Leu	
675 680 685	
cat gaa aaa gta cca ttt tgc tgc tta aga tta gac aag agt tgc caa	2112
His Glu Lys Val Pro Phe Cys Cys Leu Arg Leu Asp Lys Ser Cys Gln	
690 695 700	
cat aac tac tat gag gat gca aaa gcc tat gga ttc aaa aat aaa cta	2160
His Asn Tyr Tyr Glu Asp Ala Lys Ala Tyr Gly Phe Lys Asn Lys Leu	
705 710 715 720	
att ata gtt gca gct gaa aca gct gga aat gga tta tat aac ttt att	2208
Ile Ile Val Ala Ala Glu Thr Ala Gly Asn Gly Leu Tyr Asn Phe Ile	
725 730 735	
gtt cct ctc agg gca tat tat aga cca aag aaa gaa ctt aat ccc ata	2256
Val Pro Leu Arg Ala Tyr Tyr Arg Pro Lys Lys Glu Leu Asn Pro Ile	
740 745 750	
gta ctg cta ttg gat aac ccc cta gat gac tta ctc agg tgt gga gtg	2304
Val Leu Leu Leu Asp Asn Pro Leu Asp Asp Leu Leu Arg Cys Gly Val	
755 760 765	
act ttt gct gct aat atg gtg gtt gtg gat aaa gag agc acc atg agt	2352
Thr Phe Ala Ala Asn Met Val Val Val Asp Lys Glu Ser Thr Met Ser	
770 775 780	
gcc gag gaa gac tac atg gca gat gcc aaa acc att gtg aac gtg cag	2400
Ala Glu Glu Asp Tyr Met Ala Asp Ala Lys Thr Ile Val Asn Val Gln	
785 790 795 800	
aca ctc ttc agg ttg ttt tcc agt ctc agt att atc aca gag cta act	2448
Thr Leu Phe Arg Leu Phe Ser Ser Leu Ser Ile Ile Thr Glu Leu Thr	
805 810 815	
cac ccc gcc aac atg aga ttc atg caa ttc aga gcc aaa gac tgt tac	2496
His Pro Ala Asn Met Arg Phe Met Gln Phe Arg Ala Lys Asp Cys Tyr	
820 825 830	
tct ctt gct ctt tca aaa ctg gaa aag aaa gaa cgg gag aga ggc tct	2544
Ser Leu Ala Leu Ser Lys Leu Glu Lys Lys Glu Arg Glu Arg Gly Ser	
835 840 845	
aac ttg gcc ttt atg ttt cga ctg cct ttt gct gct ggg agg gtg ttt	2592

The "GAT" sequence

Asn	Leu	Ala	Phe	Met	Phe	Arg	Leu	Pro	Phe	Ala	Ala	Gly	Arg	Val	Phe		
850						855					860						
agc	atc	agt	atg	ttg	gac	act	ctg	ctg	tat	cag	tca	ttt	gtg	aag	gat	2640	
Ser	Ile	Ser	Met	Leu	Asp	Thr	Leu	Leu	Tyr	Gln	Ser	Phe	Val	Lys	Asp	880	
865					870					875							
tat	atg	att	tct	atc	acg	aga	ctt	ctg	ttg	gga	ctg	gac	act	aca	cca	2688	
Tyr	Met	Ile	Ser	Ile	Thr	Arg	Leu	Leu	Leu	Gly	Leu	Asp	Thr	Thr	Pro	895	
				885					890								
gga	tct	ggg	ttt	ctt	tgt	tct	atg	aaa	atc	act	gca	gat	gac	tta	tgg	2736	
Gly	Ser	Gly	Phe	Leu	Cys	Ser	Met	Lys	Ile	Thr	Ala	Asp	Asp	Leu	Trp	910	
			900					905									
atc	aga	act	tat	gcc	aga	ctt	tat	cag	aag	ttg	tgt	tct	tct	act	gga	2784	
Ile	Arg	Thr	Tyr	Ala	Arg	Leu	Tyr	Gln	Lys	Leu	Cys	Ser	Ser	Thr	Gly	925	
			915				920										
gat	gtt	ccc	att	gga	atc	tac	agg	act	gag	tct	cag	aaa	ctt	act	aca	2832	
Asp	Val	Pro	Ile	Gly	Ile	Tyr	Arg	Thr	Glu	Ser	Gln	Lys	Leu	Thr	Thr	940	
			930				935										
tct	gag	tct	cga	aaa	ata	gca	tca	caa	tct	caa	ata	tct	atc	agt	gta	2880	
Ser	Glu	Ser	Arg	Lys	Ile	Ala	Ser	Gln	Ser	Gln	Ile	Ser	Ile	Ser	Val	960	
					950					955							
gaa	gag	tgg	gaa	gac	acc	aaa	gac	tcc	aaa	gaa	caa	ggg	cac	cac	cgc	2928	
Glu	Glu	Trp	Glu	Asp	Thr	Lys	Asp	Ser	Lys	Glu	Gln	Gly	His	His	Arg	975	
				965					970								
agc	aac	cac	cgc	aac	tca	aca	tcc	agt	gac	cag	tcg	gac	cat	ccc	ttg	2976	
Ser	Asn	His	Arg	Asn	Ser	Thr	Ser	Ser	Asp	Gln	Ser	Asp	His	Pro	Leu	990	
			980					985									
ctg	cgg	aga	aaa	agc	atg	cag	tgg	gcc	cga	aga	ctg	agc	aga	aaa	ggc	3024	
Leu	Arg	Arg	Lys	Ser	Met	Gln	Trp	Ala	Arg	Arg	Leu	Ser	Arg	Lys	Gly	1005	
			995				1000										
cca	aaa	cac	tct	ggt	aaa	aca	gct	gaa	aaa	ata	acc	cag	cag	cga	ctg	3072	
Pro	Lys	His	Ser	Gly	Lys	Thr	Ala	Glu	Lys	Ile	Thr	Gln	Gln	Arg	Leu	1020	
			1010				1015										
aac	ctc	tac	agg	agg	tca	gaa	aga	caa	gag	ctt	gct	gaa	ctt	gtg	aaa	3120	
Asn	Leu	Tyr	Arg	Arg	Ser	Glu	Arg	Gln	Glu	Leu	Ala	Glu	Leu	Val	Lys	1040	
					1025		1030			1035							
aat	aga	atg	aaa	cac	ttg	ggt	ctt	tct	aca	gtg	gga	tat	gat	gaa	atg	3168	
Asn	Arg	Met	Lys	His	Leu	Gly	Leu	Ser	Thr	Val	Gly	Tyr	Asp	Glu	Met	1055	
				1045					1050								
aat	gat	cat	caa	agt	acc	ctc	tcc	tac	atc	ctg	att	aac	cca	tct	cca	3216	
Asn	Asp	His	Gln	Ser	Thr	Leu	Ser	Tyr	Ile	Leu	Ile	Asn	Pro	Ser	Pro	1070	
				1060				1065									
gat	acc	aga	ata	gag	ctg	aat	gat	gtt	gta	tac	tta	att	cga	cca	gat	3264	
Asp	Thr	Arg	Ile	Glu	Leu	Asn	Asp	Val	Val	Tyr	Leu	Ile	Arg	Pro	Asp	1085	
			1075				1080										
cca	ctg	gcc	tac	ctt	cca	aac	agt	gag	ccc	agt	cga	aga	aac	agc	atc	3312	
Pro	Leu	Ala	Tyr	Leu	Pro	Asn	Ser	Glu	Pro	Ser	Arg	Arg	Asn	Ser	Ile		

1044
 1045
 1046
 1047
 1048
 1049
 1050
 1051
 1052
 1053
 1054
 1055
 1056
 1057
 1058
 1059
 1060
 1061
 1062
 1063
 1064
 1065
 1066
 1067
 1068
 1069
 1070
 1071
 1072
 1073
 1074
 1075
 1076
 1077
 1078
 1079
 1080
 1081
 1082
 1083
 1084
 1085
 1086
 1087
 1088
 1089
 1090
 1091
 1092
 1093
 1094
 1095
 1096
 1097
 1098
 1099
 1100

1090 1095 1100

tgc aat gtc act ggt caa gat tct cgg gag gaa act caa ctt tga 3357
 Cys Asn Val Thr Gly Gln Asp Ser Arg Glu Thr Gln Leu *
 1105 1110 1115

<210> 10
 <211> 2847
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (561)...(2477)

<400> 10
 ccacgcgtcc ggccctgtgc ttcggatggc ggcgggaggt tgatggcgag tgggtgctgaa 60
 gggacagctc cagcagtggc tgatttgggg gagaaacaaa atctgcagat ggaatccgag 120
 cagggcgact tcaccttcaa gtggtgagct ctccctgacct gcggccagtc tccactccat 180
 tcacggccag ccgatctgcc cgctcccggg ggggtcgggc agtgccggct ggacccgccc 240
 cgagctccat ggtttgccc accctgcgcg atggtgactc tgggcgcgga ggttggcgac 300
 tggcaaatcc gcagatcaca gaatgaaggc ggggagcgcg gccggcggcc ggcgggggct 360
 ttctccccc cccagcgcc cagggaagcg gctcaaccac ctgaatccgg aaaacgccaa 420
 caagtagttt ctgctcggag aagggcggct cacctgggcg ccaagactca gtcccgtgc 480
 ccagagaacc tcgtccactc ggaaaccaa gcagaaccac ttttctctcg gtctcgtaa 540
 gtcattgtctg agtcacagag atg ggc aag atc gag aac aac gag agg gtg atc 593
 Met Gly Lys Ile Glu Asn Asn Glu Arg Val Ile
 1 5 10

ctc aat gtc ggg ggc acc cgg cac gaa acc tac cgc agc acc ctc aag 641
 Leu Asn Val Gly Gly Thr Arg His Glu Thr Tyr Arg Ser Thr Leu Lys
 15 20 25

acc ctg cct gga aca cgc ctg gcc ctt ctt gcc tcc tcc gag ccc cca 689
 Thr Leu Pro Gly Thr Arg Leu Ala Leu Leu Ala Ser Ser Glu Pro Pro
 30 35 40

ggc gac tgc ttg acc acg gcg ggc gac aag ctg cag ccg tcg ccg cct 737
 Gly Asp Cys Leu Thr Thr Ala Gly Asp Lys Leu Gln Pro Ser Pro Pro
 45 50 55

cca ctg tcg ccg ccg ccg aga gcg ccc ccg ctg tcc ccc ggg cca ggc 785
 Pro Leu Ser Pro Pro Pro Arg Ala Pro Pro Leu Ser Pro Gly Pro Gly
 60 65 70 75

ggc tgc ttc gag ggc ggc gcg ggc aac tgc agt tcc cgc ggc ggc agg 833
 Gly Cys Phe Glu Gly Gly Ala Gly Asn Cys Ser Ser Arg Gly Gly Arg
 80 85 90

gcc agc gac cat ccc ggt ggc ggc cgc gag ttc ttc ttc gac cgg cac 881
 Ala Ser Asp His Pro Gly Gly Gly Arg Glu Phe Phe Phe Asp Arg His
 95 100 105

ccg ggc gtc ttc gcc tat gtg ctc aat tac tac cgc acc ggc aag ctg 929
 Pro Gly Val Phe Ala Tyr Val Leu Asn Tyr Tyr Arg Thr Gly Lys Leu
 110 115 120

cac tgc ccc gca gac gtg tgc ggg ccg ctc ttc gag gag gag ctg gcc 977
 His Cys Pro Ala Asp Val Cys Gly Pro Leu Phe Glu Glu Glu Leu Ala
 125 130 135

F04640E

ttc tgg ggc atc gac gag acc gac gtg gag ccc tgc tgc tgg atg acc 1025
 Phe Trp Gly Ile Asp Glu Thr Asp Val Glu Pro Cys Cys Trp Met Thr
 140 145 150 155

tac cgg cag cac cgc gac gcc gag gag gcg ctg gac atc ttc gag acc 1073
 Tyr Arg Gln His Arg Asp Ala Glu Glu Ala Leu Asp Ile Phe Glu Thr
 160 165 170

ccc gac ctc att ggc ggc gac ccc ggc gac gac gag gac ctg gcg gcc 1121
 Pro Asp Leu Ile Gly Gly Asp Pro Gly Asp Asp Glu Asp Leu Ala Ala
 175 180 185

aag agg ctg ggc atc gag gac gcg gcg ggg ctc ggg ggc ccc gac ggc 1169
 Lys Arg Leu Gly Ile Glu Asp Ala Ala Gly Leu Gly Gly Pro Asp Gly
 190 195 200

aaa tct ggc cgc tgg agg agg ctg cag ccc cgc atg tgg gcc ctc ttc 1217
 Lys Ser Gly Arg Trp Arg Arg Leu Gln Pro Arg Met Trp Ala Leu Phe
 205 210 215

gaa gac ccc tac tgc tcc aga gcc gcc agg ttt att gct ttt gct tct 1265
 Glu Asp Pro Tyr Ser Ser Arg Ala Ala Arg Phe Ile Ala Phe Ala Ser
 220 225 230 235

tta ttc ttc atc ctg gtt tca att aca act ttt tgc ctg gaa aca cat 1313
 Leu Phe Phe Ile Leu Val Ser Ile Thr Thr Phe Cys Leu Glu Thr His
 240 245 250

gaa gct ttc aat att gtt aaa aac aag aca gaa cca gtc atc aat ggc 1361
 Glu Ala Phe Asn Ile Val Lys Asn Lys Thr Glu Pro Val Ile Asn Gly
 255 260 265

aca agt gtt gtt cta cag tat gaa att gaa acg gat cct gcc ttg acg 1409
 Thr Ser Val Val Leu Gln Tyr Glu Ile Glu Thr Asp Pro Ala Leu Thr
 270 275 280

tat gta gaa gga gtg tgt gtg gtg tgg ttt act ttt gaa ttt tta gtc 1457
 Tyr Val Glu Gly Val Cys Val Val Trp Phe Thr Phe Glu Phe Leu Val
 285 290 295

cgt att gtt ttt tca ccc aat aaa ctt gaa ttc atc aaa aat ctc ttg 1505
 Arg Ile Val Phe Ser Pro Asn Lys Leu Glu Phe Ile Lys Asn Leu Leu
 300 305 310 315

aat atc att gac ttt gtg gcc atc cta cct ttc tac tta gag gtg gga 1553
 Asn Ile Ile Asp Phe Val Ala Ile Leu Pro Phe Tyr Leu Glu Val Gly
 320 325 330

ctc agt ggg ctg tca tcc aaa gct gct aaa gat gtg ctt ggc ttc ctc 1601
 Leu Ser Gly Leu Ser Ser Lys Ala Ala Lys Asp Val Leu Gly Phe Leu
 335 340 345

agg gtg gta agg ttt gtg agg atc ctg aga att ttc aag ctc acc cgc 1649
 Arg Val Val Arg Phe Val Arg Ile Leu Arg Ile Phe Lys Leu Thr Arg
 350 355 360

cat ttt gta ggt ctg agg gtg ctt gga cat act ctt cga gct agt act 1697
 His Phe Val Gly Leu Arg Val Leu Gly His Thr Leu Arg Ala Ser Thr
 365 370 375

The "E" is a typo for "G"

Ser Lys Ala Ala Lys Asp Val Leu Gly Phe Leu Arg Val Val Arg Phe
 340 345 350
 Val Arg Ile Leu Arg Ile Phe Lys Leu Thr Arg His Phe Val Gly Leu
 355 360 365
 Arg Val Leu Gly His Thr Leu Arg Ala Ser Thr Asn Glu Phe Leu Leu
 370 375 380
 Leu Ile Ile Phe Leu Ala Leu Gly Val Leu Ile Phe Ala Thr Met Ile
 385 390 395 400
 Tyr Tyr Ala Glu Arg Val Gly Ala Gln Pro Asn Asp Pro Ser Ala Ser
 405 410 415
 Glu His Thr Gln Phe Lys Asn Ile Pro Ile Gly Phe Trp Trp Ala Val
 420 425 430
 Val Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Tyr Pro Gln Thr Trp
 435 440 445
 Ser Gly Met Leu Val Gly Ala Leu Cys Ala Leu Ala Gly Val Leu Thr
 450 455 460
 Ile Ala Met Pro Val Pro Val Ile Val Asn Asn Phe Gly Met Tyr Tyr
 465 470 475 480
 Ser Leu Ala Met Ala Lys Gln Lys Leu Pro Arg Lys Arg Lys Lys His
 485 490 495
 Ile Pro Pro Ala Pro Gln Ala Ser Ser Pro Thr Phe Cys Lys Thr Glu
 500 505 510
 Leu Asn Met Ala Cys Asn Ser Thr Gln Ser Asp Thr Cys Leu Gly Lys
 515 520 525
 Asp Asn Arg Leu Leu Glu His Asn Arg Ser Val Leu Ser Gly Asp Asp
 530 535 540
 Ser Thr Gly Ser Glu Pro Pro Leu Ser Pro Pro Glu Arg Leu Pro Ile
 545 550 555 560
 Arg Arg Ser Ser Thr Arg Asp Lys Asn Arg Arg Gly Glu Thr Cys Phe
 565 570 575
 Leu Leu Thr Thr Gly Asp Tyr Thr Cys Ala Ser Asp Gly Gly Ile Arg
 580 585 590
 Lys Gly Tyr Glu Lys Ser Arg Ser Leu Asn Asn Ile Ala Gly Leu Ala
 595 600 605
 Gly Asn Ala Leu Arg Leu Ser Pro Val Thr Ser Pro Tyr Asn Ser Pro
 610 615 620
 Cys Pro Leu Arg Arg Ser Arg Ser Pro Ile Pro Ser Ile Leu
 625 630 635

<210> 12
 <211> 1917
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1917)

<400> 12
 atg ggc aag atc gag aac aac gag agg gtg atc ctc aat gtc ggg ggc 48
 Met Gly Lys Ile Glu Asn Asn Glu Arg Val Ile Leu Asn Val Gly Gly
 1 5 10 15

 acc cgg cac gaa acc tac cgc agc acc ctc aag acc ctg cct gga aca 96
 Thr Arg His Glu Thr Tyr Arg Ser Thr Leu Lys Thr Leu Pro Gly Thr
 20 25 30

 cgc ctg gcc ctt ctt gcc tcc tcc gag ccc cca ggc gac tgc ttg acc 144
 Arg Leu Ala Leu Leu Ala Ser Ser Glu Pro Pro Gly Asp Cys Leu Thr
 35 40 45

acg gcg ggc gac aag ctg cag ccg tcg ccg cct cca ctg tcg ccg ccg	192
Thr Ala Gly Asp Lys Leu Gln Pro Ser Pro Pro Pro Leu Ser Pro Pro	
50 55 60	
ccg aga gcg ccc ccg ctg tcc ccc ggg cca ggc ggc tgc ttc gag ggc	240
Pro Arg Ala Pro Pro Leu Ser Pro Gly Pro Gly Gly Cys Phe Glu Gly	
65 70 75 80	
ggc gcg ggc aac tgc agt tcc cgc ggc ggc agg gcc agc gac cat ccc	288
Gly Ala Gly Asn Cys Ser Ser Arg Gly Gly Arg Ala Ser Asp His Pro	
85 90 95	
ggt ggc ggc cgc gag ttc ttc ttc gac cgg cac ccg ggc gtc ttc gcc	336
Gly Gly Gly Arg Glu Phe Phe Phe Asp Arg His Pro Gly Val Phe Ala	
100 105 110	
tat gtg ctc aat tac tac cgc acc ggc aag ctg cac tgc ccc gca gac	384
Tyr Val Leu Asn Tyr Tyr Arg Thr Gly Lys Leu His Cys Pro Ala Asp	
115 120 125	
gtg tgc ggg ccg ctc ttc gag gag gag ctg gcc ttc tgg ggc atc gac	432
Val Cys Gly Pro Leu Phe Glu Glu Glu Leu Ala Phe Trp Gly Ile Asp	
130 135 140	
gag acc gac gtg gag ccc tgc tgc tgg atg acc tac ccg cag cac cgc	480
Glu Thr Asp Val Glu Pro Cys Cys Trp Met Thr Tyr Arg Gln His Arg	
145 150 155 160	
gac gcc gag gag gcg ctg gac atc ttc gag acc ccc gac ctc att ggc	528
Asp Ala Glu Glu Ala Leu Asp Ile Phe Glu Thr Pro Asp Leu Ile Gly	
165 170 175	
ggc gac ccc ggc gac gac gag gac ctg gcg gcc aag agg ctg ggc atc	576
Gly Asp Pro Gly Asp Asp Glu Asp Leu Ala Ala Lys Arg Leu Gly Ile	
180 185 190	
gag gac gcg gcg ggg ctc ggg ggc ccc gac ggc aaa tct ggc cgc tgg	624
Glu Asp Ala Ala Gly Leu Gly Gly Pro Asp Gly Lys Ser Gly Arg Trp	
195 200 205	
agg agg ctg cag ccc cgc atg tgg gcc ctc ttc gaa gac ccc tac tcg	672
Arg Arg Leu Gln Pro Arg Met Trp Ala Leu Phe Glu Asp Pro Tyr Ser	
210 215 220	
tcc aga gcc gcc agg ttt att gct ttt gct tct tta ttc ttc atc ctg	720
Ser Arg Ala Ala Arg Phe Ile Ala Phe Ala Ser Leu Phe Phe Ile Leu	
225 230 235 240	
gtt tca att aca act ttt tgc ctg gaa aca cat gaa gct ttc aat att	768
Val Ser Ile Thr Thr Phe Cys Leu Glu Thr His Glu Ala Phe Asn Ile	
245 250 255	
gtt aaa aac aag aca gaa cca gtc atc aat ggc aca agt gtt gtt cta	816
Val Lys Asn Lys Thr Glu Pro Val Ile Asn Gly Thr Ser Val Val Leu	
260 265 270	
cag tat gaa att gaa acg gat cct gcc ttg acg tat gta gaa gga gtg	864
Gln Tyr Glu Ile Glu Thr Asp Pro Ala Leu Thr Tyr Val Glu Gly Val	
275 280 285	

T042433001

Asp Asn Arg Leu Leu Glu His Asn Arg Ser Val Leu Ser Gly Asp Asp
 530 535 540

agt aca gga agt gag ccg cca cta tca ccc cca gaa agg ctc ccc atc 1680
 Ser Thr Gly Ser Glu Pro Pro Leu Ser Pro Pro Glu Arg Leu Pro Ile
 545 550 555 560

aga cgc tct agt acc aga gac aaa aac aga aga ggg gaa aca tgt ttc 1728
 Arg Arg Ser Ser Thr Arg Asp Lys Asn Arg Arg Gly Glu Thr Cys Phe
 565 570 575

cta ctg acg aca ggt gat tac acg tgt gct tct gat gga ggg atc agg 1776
 Leu Leu Thr Thr Gly Asp Tyr Thr Cys Ala Ser Asp Gly Gly Ile Arg
 580 585 590

aaa gga tat gaa aaa tcc cga agc tta aac aac ata gcg ggc ttg gca 1824
 Lys Gly Tyr Glu Lys Ser Arg Ser Leu Asn Asn Ile Ala Gly Leu Ala
 595 600 605

ggc aat gct ctg agg ctc tct cca gta aca tca ccc tac aac tct cct 1872
 Gly Asn Ala Leu Arg Leu Ser Pro Val Thr Ser Pro Tyr Asn Ser Pro
 610 615 620

tgt cct ctg agg cgc tct cga tct ccc atc cca tct atc ttg taa 1917
 Cys Pro Leu Arg Arg Ser Arg Ser Pro Ile Pro Ser Ile Leu *
 625 630 635

<210> 13
 <211> 6582
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (524)...(3913)

<400> 13
 ccacgcgtcc gccacgcgt ccgccacgc gtccgagaag gcttaggtgg gcaggcagga 60
 cgagagaaag actgagagga gggaaagccg cgtaggtggg agtacagcg cgcgagggtc 120
 gagggggaac cctcgtcggt gcagatgagg aggggtgggct ttcagaacta gtccccctc 180
 gcaccccgcc ccgcccctcc cgcgctgggg tcttcacggt gccctgcctc agagcccggc 240
 tccaccacgc ccggaagagg gagtctggcc gtcggctggc tcagggcggg ccggttggct 300
 gtaccacagg tccctggccc gagtgcggga ccagagcgcg gggcggcgcg gcagccgcgg 360
 gccgaggagg ggctgcgagc gaaacggcgc ggcgcggcac ggcggacgag ttagggccgg 420
 ggcgagggag gctgtggctc ccgacagaga caggggagta gtgtcgggct gaggcgagac 480
 agcccggtag agcccagctc agcggccggc agccttcgac gcg atg ttc cgc cgg 535
 Met Phe Arg Arg
 1

agc ttg aat cgt ttt tgt gct gga gaa gag aaa cga gtt ggc aca cgc 583
 Ser Leu Asn Arg Phe Cys Ala Gly Glu Glu Lys Arg Val Gly Thr Arg
 5 10 15 20

aca gtg ttt gtt ggc aat cat cca gtt tcg gaa aca gaa gct tac att 631
 Thr Val Phe Val Gly Asn His Pro Val Ser Glu Thr Glu Ala Tyr Ile
 25 30 35

gca caa aga ttt tgt gat aat aga ata gtc tca tct aag tat aca ctt 679
 Ala Gln Arg Phe Cys Asp Asn Arg Ile Val Ser Ser Lys Tyr Thr Leu
 40 45 50

The sequence is identical to the sequence in the GenBank database.

tgg aat ttt ctc cca aag aat ctg ttt gaa cag ttt aga aga att gca 727
 Trp Asn Phe Leu Pro Lys Asn Leu Phe Glu Gln Phe Arg Arg Ile Ala
 55 60 65

aat ttt tat ttt ctc ata atc ttc ctt gta cag gtc aca gta gac aca 775
 Asn Phe Tyr Phe Leu Ile Ile Phe Leu Val Gln Val Thr Val Asp Thr
 70 75 80

cca act agc cca gtt acc agt gga ctt cca ctt ttc ttt gtt ata act 823
 Pro Thr Ser Pro Val Thr Ser Gly Leu Pro Leu Phe Phe Val Ile Thr
 85 90 95 100

gtt aca gcc atc aag cag gga tat gag gat tgg ctg aga cac aga gct 871
 Val Thr Ala Ile Lys Gln Gly Tyr Glu Asp Trp Leu Arg His Arg Ala
 105 110 115

gac aat gaa gtc aac aaa agc act gtt tac att att gaa aat gca aag 919
 Asp Asn Glu Val Asn Lys Ser Thr Val Tyr Ile Ile Glu Asn Ala Lys
 120 125 130

cga gtg aga aaa gaa agt gaa aaa atc aag gtt ggt gat gta gta gaa 967
 Arg Val Arg Lys Glu Ser Glu Lys Ile Lys Val Gly Asp Val Val Glu
 135 140 145

gta cag gca gat gaa acc ttt ccc tgt gat ctt att ctt cta tca tct 1015
 Val Gln Ala Asp Glu Thr Phe Pro Cys Asp Leu Ile Leu Leu Ser Ser
 150 155 160

tgc acc act gat gga acc tgt tat gtc act aca gcc agt ctt gat ggg 1063
 Cys Thr Thr Asp Gly Thr Cys Tyr Val Thr Thr Ala Ser Leu Asp Gly
 165 170 175 180

gaa tcc aat tgc aag aca cat tat gca gta cgt gat acc att gca ctg 1111
 Glu Ser Asn Cys Lys Thr His Tyr Ala Val Arg Asp Thr Ile Ala Leu
 185 190 195

tgt aca gca gaa tcc atc gat acc ctc cga gca gca att gaa tgt gaa 1159
 Cys Thr Ala Glu Ser Ile Asp Thr Leu Arg Ala Ala Ile Glu Cys Glu
 200 205 210

cag cct caa cct gac ctc tac aaa ttt gtt ggg cga atc aat atc tac 1207
 Gln Pro Gln Pro Asp Leu Tyr Lys Phe Val Gly Arg Ile Asn Ile Tyr
 215 220 225

agt aat agt ctt gag gct gtt gcc agg tct ttg gga cct gaa aat ctc 1255
 Ser Asn Ser Leu Glu Ala Val Ala Arg Ser Leu Gly Pro Glu Asn Leu
 230 235 240

ttg ctg aaa gga gct acg cta aaa aat acc gag aag ata tat gga gtt 1303
 Leu Leu Lys Gly Ala Thr Leu Lys Asn Thr Glu Lys Ile Tyr Gly Val
 245 250 255 260

gct gtt tac act gga atg gaa acc aaa atg gct ttg aac tac caa ggg 1351
 Ala Val Tyr Thr Gly Met Glu Thr Lys Met Ala Leu Asn Tyr Gln Gly
 265 270 275

aaa tct cag aaa cgt tct gct gtt gaa aaa tct att aat gct ttc ctg 1399
 Lys Ser Gln Lys Arg Ser Ala Val Glu Lys Ser Ile Asn Ala Phe Leu
 280 285 290

1004629 431304
 T004629 431304

att gta tat tta ttt atc tta ctg acc aaa gct gca gta tgc act act 1447
 Ile Val Tyr Leu Phe Ile Leu Leu Thr Lys Ala Ala Val Cys Thr Thr
 295 300 305

cta aag tat gtt tgg caa agt acc cca tac aat gat gaa cct tgg tat 1495
 Leu Lys Tyr Val Trp Gln Ser Thr Pro Tyr Asn Asp Glu Pro Trp Tyr
 310 315 320

aac caa aag act cag aaa gag cga gag acc ttg aag gtt tta aaa atg 1543
 Asn Gln Lys Thr Gln Lys Glu Arg Glu Thr Leu Lys Val Leu Lys Met
 325 330 335 340

ttc acc gac ttc cta tca ttt atg gtt cta ttc aac ttt atc att cct 1591
 Phe Thr Asp Phe Leu Ser Phe Met Val Leu Phe Asn Phe Ile Ile Pro
 345 350 355

gtc tcc atg tac gtc aca gta gaa atg cag aaa ttc ttg ggc tcc ttc 1639
 Val Ser Met Tyr Val Thr Val Glu Met Gln Lys Phe Leu Gly Ser Phe
 360 365 370

ttc atc tca tgg gat aag gac ttt tat gat gaa gaa att aat gaa gga 1687
 Phe Ile Ser Trp Asp Lys Asp Phe Tyr Asp Glu Glu Ile Asn Glu Gly
 375 380 385

gcc ctg gtt aac aca tca gac ctt aat gaa gaa ctt ggt cag gtg gat 1735
 Ala Leu Val Asn Thr Ser Asp Leu Asn Glu Glu Leu Gly Gln Val Asp
 390 395 400

tat gta ttt aca gat aag act gga aca ctc act gaa aac agc atg gaa 1783
 Tyr Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu Asn Ser Met Glu
 405 410 415 420

ttc att gaa tgc tgc ata gat ggc cac aaa tat aaa ggt gta act caa 1831
 Phe Ile Glu Cys Cys Ile Asp Gly His Lys Tyr Lys Gly Val Thr Gln
 425 430 435

gag gtt gat gga tta tct caa act gat gga act tta aca tat ttt gac 1879
 Glu Val Asp Gly Leu Ser Gln Thr Asp Gly Thr Leu Thr Tyr Phe Asp
 440 445 450

aaa gta gat aag aat cga gaa gag ctg ttt cta cgt gcc ttg tgt tta 1927
 Lys Val Asp Lys Asn Arg Glu Glu Leu Phe Leu Arg Ala Leu Cys Leu
 455 460 465

tgt cat act gta gaa atc aaa aca aac gat gct gtt gat gga gct aca 1975
 Cys His Thr Val Glu Ile Lys Thr Asn Asp Ala Val Asp Gly Ala Thr
 470 475 480

gaa tca gct gaa tta acc tat atc tcc tct tca cca gat gaa ata gct 2023
 Glu Ser Ala Glu Leu Thr Tyr Ile Ser Ser Ser Pro Asp Glu Ile Ala
 485 490 495 500

ttg gtg aaa gga gct aaa agg tac ggg ttc aca ttt tta gga aat cga 2071
 Leu Val Lys Gly Ala Lys Arg Tyr Gly Phe Thr Phe Leu Gly Asn Arg
 505 510 515

aat gga tat atg aga gta gag aac caa aga aaa gaa ata gaa gaa tat 2119
 Asn Gly Tyr Met Arg Val Glu Asn Gln Arg Lys Glu Ile Glu Glu Tyr
 520 525 530

gaa ctt ctt cac acc tta aac ttt gat gct gtc cgg cga cgt atg agt 2167

Glu Leu Leu His Thr Leu Asn Phe Asp Ala Val Arg Arg Arg Met Ser
 535 540 545
 gta att gtg aag act caa gaa gga gac ata ctt ctc ttt tgt aaa gga 2215
 Val Ile Val Lys Thr Gln Glu Gly Asp Ile Leu Leu Phe Cys Lys Gly
 550 555 560
 gca gac tcg gca gtt ttt ccc aga gtg caa aat cat gaa att gag tta 2263
 Ala Asp Ser Ala Val Phe Pro Arg Val Gln Asn His Glu Ile Glu Leu
 565 570 575 580
 act aaa gtc cat gtg gaa cgt aat gca atg gat ggg tat cgg aca ctc 2311
 Thr Lys Val His Val Glu Arg Asn Ala Met Asp Gly Tyr Arg Thr Leu
 585 590 595
 tgt gta gcc ttc aaa gaa att gct cca gat gat tat gaa aga att aac 2359
 Cys Val Ala Phe Lys Glu Ile Ala Pro Asp Asp Tyr Glu Arg Ile Asn
 600 605 610
 aga cag ctc ata gag gca aaa atg gcc tta caa gac aga gaa gaa aaa 2407
 Arg Gln Leu Ile Glu Ala Lys Met Ala Leu Gln Asp Arg Glu Glu Lys
 615 620 625
 atg gaa aaa gtt ttc gat gat att gag aca aac atg aat tta att gga 2455
 Met Glu Lys Val Phe Asp Asp Ile Glu Thr Asn Met Asn Leu Ile Gly
 630 635 640
 gcc act gca gtt gaa gac aag cta caa gat caa gct gca gag acc att 2503
 Ala Thr Ala Val Glu Asp Lys Leu Gln Asp Gln Ala Ala Glu Thr Ile
 645 650 655 660
 gaa gct ctg cat gca gca ggc ctg aaa gtc tgg gtg ctc act ggg gac 2551
 Glu Ala Leu His Ala Ala Gly Leu Lys Val Trp Val Leu Thr Gly Asp
 665 670 675
 aag atg gag aca gct aaa tcc aca tgc tat gcc tgc cgc ctt ttc cag 2599
 Lys Met Glu Thr Ala Lys Ser Thr Cys Tyr Ala Cys Arg Leu Phe Gln
 680 685 690
 acc aac act gag ctc tta gaa cta acc aca aaa acc att gaa gaa agt 2647
 Thr Asn Thr Glu Leu Leu Glu Leu Thr Thr Lys Thr Ile Glu Glu Ser
 695 700 705
 gaa agg aaa gaa gat cga tta cat gaa tta ttg ata gaa tat cgc aag 2695
 Glu Arg Lys Glu Asp Arg Leu His Glu Leu Leu Ile Glu Tyr Arg Lys
 710 715 720
 aaa ttg ctg cat gag ttt cct aaa agt act aga agc ttt aaa aaa gca 2743
 Lys Leu Leu His Glu Phe Pro Lys Ser Thr Arg Ser Phe Lys Lys Ala
 725 730 735 740
 tgg aca gaa cat cag gaa tat gga tta atc ata gat ggc tcc aca ttg 2791
 Trp Thr Glu His Gln Glu Tyr Gly Leu Ile Ile Asp Gly Ser Thr Leu
 745 750 755
 tca ctc ata cta aat tct agt caa gac tct agt tca aac aat tac aaa 2839
 Ser Leu Ile Leu Asn Ser Ser Gln Asp Ser Ser Ser Asn Asn Tyr Lys
 760 765 770
 agc att ttc cta caa ata tgt atg aag tgt act gca gtg ctc tgc tgt 2887
 Ser Ile Phe Leu Gln Ile Cys Met Lys Cys Thr Ala Val Leu Cys Cys

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100

775	780	785	
cgg atg gca cca tta cag aaa gcc cag att gtc aga atg gtg aag aat			2935
Arg Met Ala Pro Leu Gln Lys Ala Gln Ile Val Arg Met Val Lys Asn			
790	795	800	
tta aaa ggc agc cca ata act ctg tcg ata ggt gat ggt gcc aat gat			2983
Leu Lys Gly Ser Pro Ile Thr Leu Ser Ile Gly Asp Gly Ala Asn Asp			
805	810	815	820
gtt agt atg atc ttg gaa tcc cat gtg gga ata ggt att aaa ggc aaa			3031
Val Ser Met Ile Leu Glu Ser His Val Gly Ile Gly Ile Lys Gly Lys			
	825	830	835
gaa ggt cgc caa gca gct agg aat agc gat tat tct gtt cca aag ttt			3079
Glu Gly Arg Gln Ala Ala Arg Asn Ser Asp Tyr Ser Val Pro Lys Phe			
	840	845	850
aaa cac tta aag aaa ctg ctg ttg gct cat gga cat cta tat tat gtg			3127
Lys His Leu Lys Lys Leu Leu Leu Ala His Gly His Leu Tyr Tyr Val			
	855	860	865
aga ata gca cac ctt gta cag tac ttc ttc tat aag aac ctt tgt ttc			3175
Arg Ile Ala His Leu Val Gln Tyr Phe Phe Tyr Lys Asn Leu Cys Phe			
	870	875	880
att ttg cca cag ttt ttg tac cag ttc ttc tgt gga ttc tca caa cag			3223
Ile Leu Pro Gln Phe Leu Tyr Gln Phe Phe Cys Gly Phe Ser Gln Gln			
	885	890	900
cca ctg tat gat gct gct tac ctt aca atg tac aat atc tgc ttc aca			3271
Pro Leu Tyr Asp Ala Ala Tyr Leu Thr Met Tyr Asn Ile Cys Phe Thr			
	905	910	915
tcc ttg ccc atc ctg gcc tat agt cta ctg gaa cag cac atc aac att			3319
Ser Leu Pro Ile Leu Ala Tyr Ser Leu Leu Glu Gln His Ile Asn Ile			
	920	925	930
gac act ctg acc tca gat ccc cga ttg tat atg aaa att tct ggc aat			3367
Asp Thr Leu Thr Ser Asp Pro Arg Leu Tyr Met Lys Ile Ser Gly Asn			
	935	940	945
gcc atg cta cag ttg ggc ccc ttc tta tat tgg aca ttt ctg gct gcc			3415
Ala Met Leu Gln Leu Gly Pro Phe Leu Tyr Trp Thr Phe Leu Ala Ala			
	950	955	960
ttt gaa ggg aca gtg ttc ttc ttt ggg act tac ttt ctt ttt cag act			3463
Phe Glu Gly Thr Val Phe Phe Phe Gly Thr Tyr Phe Leu Phe Gln Thr			
	965	970	975
gca tcc cta gaa gaa aat gga aag gta tac gga aac tgg act ttt gga			3511
Ala Ser Leu Glu Glu Asn Gly Lys Val Tyr Gly Asn Trp Thr Phe Gly			
	985	990	995
acc att gtt ttt aca gtc tta gta ttc act gta acc ctg aag ctt gcc			3559
Thr Ile Val Phe Thr Val Leu Val Phe Thr Val Thr Leu Lys Leu Ala			
	1000	1005	1010
ttg gat acc cga ttc tgg acg tgg ata aat cac ttt gtg att tgg ggt			3607
Leu Asp Thr Arg Phe Trp Thr Trp Ile Asn His Phe Val Ile Trp Gly			
	1015	1020	1025

T00463 22942001

tct tta gcc ttc tat gta ttt ttc tca ttc ttc tgg gga gga att att 3655
 Ser Leu Ala Phe Tyr Val Phe Phe Ser Phe Phe Trp Gly Gly Ile Ile
 1030 1035 1040

tgg cct ttt ctc aag caa cag aga atg tat ttt gta ttt gcc caa atg 3703
 Trp Pro Phe Leu Lys Gln Gln Arg Met Tyr Phe Val Phe Ala Gln Met
 1045 1050 1055 1060

ctg tct tct gta tcc aca tgg ttg gct ata att ctt cta ata ttt atc 3751
 Leu Ser Ser Val Ser Thr Trp Leu Ala Ile Ile Leu Leu Ile Phe Ile
 1065 1070 1075

agc ctg ttc cct gag att ctt ctg ata gta tta aag aat gta aga aga 3799
 Ser Leu Phe Pro Glu Ile Leu Leu Ile Val Leu Lys Asn Val Arg Arg
 1080 1085 1090

aga agt gcc agg aga aat ctg agc tgt aga agg gca tct gac tca tta 3847
 Arg Ser Ala Arg Arg Asn Leu Ser Cys Arg Arg Ala Ser Asp Ser Leu
 1095 1100 1105

tcc gcc aga cct tca gtc aga cct ctt ctt tta cga aca ttc tca gac 3895
 Ser Ala Arg Pro Ser Val Arg Pro Leu Leu Leu Arg Thr Phe Ser Asp
 1110 1115 1120

gaa tct aat gta ttg taa cagaatccga atcttgaact gcctatgita 3943
 Glu Ser Asn Val Leu *
 1125

ttgtcctaca agcatactga cagtgggttac agctaaaaaa gaaagcatga agaaacaact 4003
 acaaaaagtt atcatctcag gatacttgat atgcaacaca ctaaaccact ctcatgtcta 4063
 gagttcacaa taaatgttca ttaaaatacc aaatgattct cttaagcatt taccattatt 4123
 gtaagtagcc tttatggcca aagctgtaag ttaagaatta tatgaaagtt gaaagcaaga 4183
 atacttagaa ttctggcttt agttagagta atataactca aatgggtgct cttttaaccc 4243
 atgaactttg tgaatggatt taaatacaat agtatgaagt agaagttatg caatgagaat 4303
 gaatagattt tgctaatact actttttttg cctggcagaa gaaatagact atttgatca 4363
 cattttctcat tctcctaa tgatcatctt aatttttttt cccaagtaca taaggaatac 4423
 ttgaaaatac agaataacta aatagtatca atgcatcaga cagaatagtt aatcccttct 4483
 gtttaccat gtgctactaa tgtcttggtta gaatattctt gccaaaaaaa taccttgaac 4543
 gcttatgtgg aaagtgttaa cttacgggta tttttgtggg aatagaaaaa aattgtttat 4603
 tttttattct tctgaattaa accccactta tgggtgtaag cctactagac ttgaaaataa 4663
 agtataaaac atttccaatc acttagtagc cctcaaaagt agttagaaaa taaacagatt 4723
 tttccagtgt tgattttact gggatctgca gtaaggtggt ttaaaccata gttatataaa 4783
 aataaaggtc attctgaata tcagcctttt ataattttat gtgaagagga agaaatatag 4843
 cttatttttaa acttttgacg gttttttatt gaaagagatt gcatttatgc atatatgcag 4903
 tgctttttct taaacttggc caatttgtaa agggggaagg agccacccca aaacgggtggt 4963
 tcagcttgta gagccatgac tctgtgaaga tgaatgttgt ctcttaactt ggacagggaa 5023
 atggtctaac tctaaaccat gtaactgacc ttagtaaaagt ccttgactaa ctgaactaga 5083
 aggaagggtt agccttctaa ttagttcact tgaaacataa atgtgaaatg tottcattca 5143
 atgttaaaca catacttttt tggatataaa tgaccatatt tatttgactg ctagtttttt 5203
 tgtttttttt ttgtctttct ggcattgctg tactattatt aatgtttata ttgtaccttg 5263
 atttggaata gtattggagt taatctgtat tatatttata tagtccatat ggcacatttg 5323
 attcttcac atataatttg tgttaatggt taggtatgat ttttttctaa attctagaaa 5383
 agaacataat ttcagttatc agaagccatt ccatcattat agaccctttt tcattatttc 5443
 atttgctctc atatatcagt attatttttg agcattttgt tacatgtcat tcacaactta 5503
 cctaagtgtg ctgtgttctg gtagcccgta tttgaggtaa gctgctgaaa acaaaagtct 5563
 ctatattctt tgcctattcc aaagagctaa aaaagtctaa ccagaggaaag cttttgatatt 5623
 tttgtgtttg ttttcttggt cttatgggtt ttgttgctgt attatgattg ctgtttttaca 5683
 taaaatctat gggaaactgtg aatacagaca agagagccac agtagagagg cttgtttta 5743
 gcagtaccat tggagagtta acagaataat ctagtagaaa aataactggt tgcattgaaa 5803
 attccttcca gccagaaaga aagaaagaca aggagtaagg gggatttga gttatgtctc 5863

10045
 10046
 10047
 10048
 10049
 10050
 10051
 10052
 10053
 10054
 10055
 10056
 10057
 10058
 10059
 10060
 10061
 10062
 10063
 10064
 10065
 10066
 10067
 10068
 10069
 10070
 10071
 10072
 10073
 10074
 10075
 10076
 10077
 10078
 10079
 10080
 10081
 10082
 10083
 10084
 10085
 10086
 10087
 10088
 10089
 10090
 10091
 10092
 10093
 10094
 10095
 10096
 10097
 10098
 10099
 10100

Val Leu Lys Met Phe Thr Asp Phe Leu Ser Phe Met Val Leu Phe Asn
 340 345 350
 Phe Ile Ile Pro Val Ser Met Tyr Val Thr Val Glu Met Gln Lys Phe
 355 360 365
 Leu Gly Ser Phe Phe Ile Ser Trp Asp Lys Asp Phe Tyr Asp Glu Glu
 370 375 380
 Ile Asn Glu Gly Ala Leu Val Asn Thr Ser Asp Leu Asn Glu Glu Leu
 385 390 395 400
 Gly Gln Val Asp Tyr Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu
 405 410 415
 Asn Ser Met Glu Phe Ile Glu Cys Cys Ile Asp Gly His Lys Tyr Lys
 420 425 430
 Gly Val Thr Gln Glu Val Asp Gly Leu Ser Gln Thr Asp Gly Thr Leu
 435 440 445
 Thr Tyr Phe Asp Lys Val Asp Lys Asn Arg Glu Glu Leu Phe Leu Arg
 450 455 460
 Ala Leu Cys Leu Cys His Thr Val Glu Ile Lys Thr Asn Asp Ala Val
 465 470 475 480
 Asp Gly Ala Thr Glu Ser Ala Glu Leu Thr Tyr Ile Ser Ser Ser Pro
 485 490 495
 Asp Glu Ile Ala Leu Val Lys Gly Ala Lys Arg Tyr Gly Phe Thr Phe
 500 505 510
 Leu Gly Asn Arg Asn Gly Tyr Met Arg Val Glu Asn Gln Arg Lys Glu
 515 520 525
 Ile Glu Glu Tyr Glu Leu Leu His Thr Leu Asn Phe Asp Ala Val Arg
 530 535 540
 Arg Arg Met Ser Val Ile Val Lys Thr Gln Glu Gly Asp Ile Leu Leu
 545 550 555 560
 Phe Cys Lys Gly Ala Asp Ser Ala Val Phe Pro Arg Val Gln Asn His
 565 570 575
 Glu Ile Glu Leu Thr Lys Val His Val Glu Arg Asn Ala Met Asp Gly
 580 585 590
 Tyr Arg Thr Leu Cys Val Ala Phe Lys Glu Ile Ala Pro Asp Asp Tyr
 595 600 605
 Glu Arg Ile Asn Arg Gln Leu Ile Glu Ala Lys Met Ala Leu Gln Asp
 610 615 620
 Arg Glu Glu Lys Met Glu Lys Val Phe Asp Asp Ile Glu Thr Asn Met
 625 630 635 640
 Asn Leu Ile Gly Ala Thr Ala Val Glu Asp Lys Leu Gln Asp Gln Ala
 645 650 655
 Ala Glu Thr Ile Glu Ala Leu His Ala Ala Gly Leu Lys Val Trp Val
 660 665 670
 Leu Thr Gly Asp Lys Met Glu Thr Ala Lys Ser Thr Cys Tyr Ala Cys
 675 680 685
 Arg Leu Phe Gln Thr Asn Thr Glu Leu Leu Glu Leu Thr Thr Lys Thr
 690 695 700
 Ile Glu Glu Ser Glu Arg Lys Glu Asp Arg Leu His Glu Leu Leu Ile
 705 710 715 720
 Glu Tyr Arg Lys Lys Leu Leu His Glu Phe Pro Lys Ser Thr Arg Ser
 725 730 735
 Phe Lys Lys Ala Trp Thr Glu His Gln Glu Tyr Gly Leu Ile Ile Asp
 740 745 750
 Gly Ser Thr Leu Ser Leu Ile Leu Asn Ser Ser Gln Asp Ser Ser Ser
 755 760 765
 Asn Asn Tyr Lys Ser Ile Phe Leu Gln Ile Cys Met Lys Cys Thr Ala
 770 775 780
 Val Leu Cys Cys Arg Met Ala Pro Leu Gln Lys Ala Gln Ile Val Arg
 785 790 795 800
 Met Val Lys Asn Leu Lys Gly Ser Pro Ile Thr Leu Ser Ile Gly Asp
 805 810 815
 Gly Ala Asn Asp Val Ser Met Ile Leu Glu Ser His Val Gly Ile Gly

T
O
T
A
L
C
O
U
N
T

820 825 830
 Ile Lys Gly Lys Glu Gly Arg Gln Ala Ala Arg Asn Ser Asp Tyr Ser
 835 840 845
 Val Pro Lys Phe Lys His Leu Lys Lys Leu Leu Leu Ala His Gly His
 850 855 860
 Leu Tyr Tyr Val Arg Ile Ala His Leu Val Gln Tyr Phe Phe Tyr Lys
 865 870 875 880
 Asn Leu Cys Phe Ile Leu Pro Gln Phe Leu Tyr Gln Phe Phe Cys Gly
 885 890 895
 Phe Ser Gln Gln Pro Leu Tyr Asp Ala Ala Tyr Leu Thr Met Tyr Asn
 900 905 910
 Ile Cys Phe Thr Ser Leu Pro Ile Leu Ala Tyr Ser Leu Leu Glu Gln
 915 920 925
 His Ile Asn Ile Asp Thr Leu Thr Ser Asp Pro Arg Leu Tyr Met Lys
 930 935 940
 Ile Ser Gly Asn Ala Met Leu Gln Leu Gly Pro Phe Leu Tyr Trp Thr
 945 950 955 960
 Phe Leu Ala Ala Phe Glu Gly Thr Val Phe Phe Phe Gly Thr Tyr Phe
 965 970 975
 Leu Phe Gln Thr Ala Ser Leu Glu Glu Asn Gly Lys Val Tyr Gly Asn
 980 985 990
 Trp Thr Phe Gly Thr Ile Val Phe Thr Val Leu Val Phe Thr Val Thr
 995 1000 1005
 Leu Lys Leu Ala Leu Asp Thr Arg Phe Trp Thr Trp Ile Asn His Phe
 1010 1015 1020
 Val Ile Trp Gly Ser Leu Ala Phe Tyr Val Phe Phe Ser Phe Phe Trp
 1025 1030 1035 1040
 Gly Gly Ile Ile Trp Pro Phe Leu Lys Gln Gln Arg Met Tyr Phe Val
 1045 1050 1055
 Phe Ala Gln Met Leu Ser Ser Val Ser Thr Trp Leu Ala Ile Ile Leu
 1060 1065 1070
 Leu Ile Phe Ile Ser Leu Phe Pro Glu Ile Leu Leu Ile Val Leu Lys
 1075 1080 1085
 Asn Val Arg Arg Arg Ser Ala Arg Arg Asn Leu Ser Cys Arg Arg Ala
 1090 1095 1100
 Ser Asp Ser Leu Ser Ala Arg Pro Ser Val Arg Pro Leu Leu Leu Arg
 1105 1110 1115 1120
 Thr Phe Ser Asp Glu Ser Asn Val Leu
 1125

<210> 15

<211> 3390

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(3390)

<400> 15

atg ttc cgc cgg agc ttg aat cgt ttt tgt gct gga gaa gag aaa cga 48
 Met Phe Arg Arg Ser Leu Asn Arg Phe Cys Ala Gly Glu Glu Lys Arg
 1 5 10 15
 gtt ggc aca cgc aca gtg ttt gtt ggc aat cat cca gtt tcg gaa aca 96
 Val Gly Thr Arg Thr Val Phe Val Gly Asn His Pro Val Ser Glu Thr
 20 25 30
 gaa gct tac att gca caa aga ttt tgt gat aat aga ata gtc tca tct 144
 Glu Ala Tyr Ile Ala Gln Arg Phe Cys Asp Asn Arg Ile Val Ser Ser

35	40	45	
aag tat aca ctt tgg aat ttt ctc cca aag aat ctg ttt gaa cag ttt Lys Tyr Thr Leu Trp Asn Phe Leu Pro Lys Asn Leu Phe Glu Gln Phe 50 55 60			192
aga aga att gca aat ttt tat ttt ctc ata atc ttc ctt gta cag gtc Arg Arg Ile Ala Asn Phe Tyr Phe Leu Ile Ile Phe Leu Val Gln Val 65 70 75 80			240
aca gta gac aca cca act agc cca gtt acc agt gga ctt cca ctt ttc Thr Val Asp Thr Pro Thr Ser Pro Val Thr Ser Gly Leu Pro Leu Phe 85 90 95			288
ttt gtt ata act gtt aca gcc atc aag cag gga tat gag gat tgg ctg Phe Val Ile Thr Val Thr Ala Ile Lys Gln Gly Tyr Glu Asp Trp Leu 100 105 110			336
aga cac aga gct gac aat gaa gtc aac aaa agc act gtt tac att att Arg His Arg Ala Asp Asn Glu Val Asn Lys Ser Thr Val Tyr Ile Ile 115 120 125			384
gaa aat gca aag cga gtg aga aaa gaa agt gaa aaa atc aag gtt ggt Glu Asn Ala Lys Arg Val Arg Lys Glu Ser Glu Lys Ile Lys Val Gly 130 135 140			432
gat gta gta gaa gta cag gca gat gaa acc ttt ccc tgt gat ctt att Asp Val Val Glu Val Gln Ala Asp Glu Thr Phe Pro Cys Asp Leu Ile 145 150 155 160			480
ctt cta tca tct tgc acc act gat gga acc tgt tat gtc act aca gcc Leu Leu Ser Ser Cys Thr Thr Asp Gly Thr Cys Tyr Val Thr Thr Ala 165 170 175			528
agt ctt gat ggg gaa tcc aat tgc aag aca cat tat gca gta cgt gat Ser Leu Asp Gly Glu Ser Asn Cys Lys Thr His Tyr Ala Val Arg Asp 180 185 190			576
acc att gca ctg tgt aca gca gaa tcc atc gat acc ctc cga gca gca Thr Ile Ala Leu Cys Thr Ala Glu Ser Ile Asp Thr Leu Arg Ala Ala 195 200 205			624
att gaa tgt gaa cag cct caa cct gac ctc tac aaa ttt gtt ggg cga Ile Glu Cys Glu Gln Pro Gln Pro Asp Leu Tyr Lys Phe Val Gly Arg 210 215 220			672
atc aat atc tac agt aat agt ctt gag gct gtt gcc agg tct ttg gga Ile Asn Ile Tyr Ser Asn Ser Leu Glu Ala Val Ala Arg Ser Leu Gly 225 230 235 240			720
cct gaa aat ctc ttg ctg aaa gga gct acg cta aaa aat acc gag aag Pro Glu Asn Leu Leu Leu Lys Gly Ala Thr Leu Lys Asn Thr Glu Lys 245 250 255			768
ata tat gga gtt gct gtt tac act gga atg gaa acc aaa atg gct ttg Ile Tyr Gly Val Ala Val Tyr Thr Gly Met Glu Thr Lys Met Ala Leu 260 265 270			816
aac tac caa ggg aaa tct cag aaa cgt tct gct gtt gaa aaa tct att Asn Tyr Gln Gly Lys Ser Gln Lys Arg Ser Ala Val Glu Lys Ser Ile 275 280 285			864

aat gct ttc ctg att gta tat tta ttt atc tta ctg acc aaa gct gca	912
Asn Ala Phe Leu Ile Val Tyr Leu Phe Ile Leu Leu Thr Lys Ala Ala	
290 295 300	
gta tgc act act cta aag tat gtt tgg caa agt acc cca tac aat gat	960
Val Cys Thr Thr Leu Lys Tyr Val Trp Gln Ser Thr Pro Tyr Asn Asp	
305 310 315 320	
gaa cct tgg tat aac caa aag act cag aaa gag cga gag acc ttg aag	1008
Glu Pro Trp Tyr Asn Gln Lys Thr Gln Lys Glu Arg Glu Thr Leu Lys	
325 330 335	
gtt tta aaa atg ttc acc gac ttc cta tca ttt atg gtt cta ttc aac	1056
Val Leu Lys Met Phe Thr Asp Phe Leu Ser Phe Met Val Leu Phe Asn	
340 345 350	
ttt atc att cct gtc tcc atg tac gtc aca gta gaa atg cag aaa ttc	1104
Phe Ile Ile Pro Val Ser Met Tyr Val Thr Val Glu Met Gln Lys Phe	
355 360 365	
ttg ggc tcc ttc ttc atc tca tgg gat aag gac ttt tat gat gaa gaa	1152
Leu Gly Ser Phe Phe Ile Ser Trp Asp Lys Asp Phe Tyr Asp Glu Glu	
370 375 380	
att aat gaa gga gcc ctg gtt aac aca tca gac ctt aat gaa gaa ctt	1200
Ile Asn Glu Gly Ala Leu Val Asn Thr Ser Asp Leu Asn Glu Glu Leu	
385 390 395 400	
ggt cag gtg gat tat gta ttt aca gat aag act gga aca ctc act gaa	1248
Gly Gln Val Asp Tyr Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu	
405 410 415	
aac agc atg gaa ttc att gaa tgc tgc ata gat ggc cac aaa tat aaa	1296
Asn Ser Met Glu Phe Ile Glu Cys Cys Ile Asp Gly His Lys Tyr Lys	
420 425 430	
ggt gta act caa gag gtt gat gga tta tct caa act gat gga act tta	1344
Gly Val Thr Gln Glu Val Asp Gly Leu Ser Gln Thr Asp Gly Thr Leu	
435 440 445	
aca tat ttt gac aaa gta gat aag aat cga gaa gag ctg ttt cta cgt	1392
Thr Tyr Phe Asp Lys Val Asp Lys Asn Arg Glu Glu Leu Phe Leu Arg	
450 455 460	
gcc ttg tgt tta tgt cat act gta gaa atc aaa aca aac gat gct gtt	1440
Ala Leu Cys Leu Cys His Thr Val Glu Ile Lys Thr Asn Asp Ala Val	
465 470 475 480	
gat gga gct aca gaa tca gct gaa tta acc tat atc tcc tct tca cca	1488
Asp Gly Ala Thr Glu Ser Ala Glu Leu Thr Tyr Ile Ser Ser Ser Pro	
485 490 495	
gat gaa ata gct ttg gtg aaa gga gct aaa agg tac ggg ttc aca ttt	1536
Asp Glu Ile Ala Leu Val Lys Gly Ala Lys Arg Tyr Gly Phe Thr Phe	
500 505 510	
tta gga aat cga aat gga tat atg aga gta gag aac caa aga aaa gaa	1584
Leu Gly Asn Arg Asn Gly Tyr Met Arg Val Glu Asn Gln Arg Lys Glu	
515 520 525	

ata gaa gaa tat gaa ctt ctt cac acc tta aac ttt gat gct gtc cgg	1632
Ile Glu Glu Tyr Glu Leu Leu His Thr Leu Asn Phe Asp Ala Val Arg	
530 535 540	
cga cgt atg agt gta att gtg aag act caa gaa gga gac ata ctt ctc	1680
Arg Arg Met Ser Val Ile Val Lys Thr Gln Glu Gly Asp Ile Leu Leu	
545 550 555 560	
ttt tgt aaa gga gca gac tcg gca gtt ttt ccc aga gtg caa aat cat	1728
Phe Cys Lys Gly Ala Asp Ser Ala Val Phe Pro Arg Val Gln Asn His	
565 570 575	
gaa att gag tta act aaa gtc cat gtg gaa cgt aat gca atg gat ggg	1776
Glu Ile Glu Leu Thr Lys Val His Val Glu Arg Asn Ala Met Asp Gly	
580 585 590	
tat cgg aca ctc tgt gta gcc ttc aaa gaa att gct cca gat gat tat	1824
Tyr Arg Thr Leu Cys Val Ala Phe Lys Glu Ile Ala Pro Asp Asp Tyr	
595 600 605	
gaa aga att aac aga cag ctc ata gag gca aaa atg gcc tta caa gac	1872
Glu Arg Ile Asn Arg Gln Leu Ile Glu Ala Lys Met Ala Leu Gln Asp	
610 615 620	
aga gaa gaa aaa atg gaa aaa gtt ttc gat gat att gag aca aac atg	1920
Arg Glu Glu Lys Met Glu Lys Val Phe Asp Asp Ile Glu Thr Asn Met	
625 630 635 640	
aat tta att gga gcc act gca gtt gaa gac aag cta caa gat caa gct	1968
Asn Leu Ile Gly Ala Thr Ala Val Glu Asp Lys Leu Gln Asp Gln Ala	
645 650 655	
gca gag acc att gaa gct ctg cat gca gca ggc ctg aaa gtc tgg gtg	2016
Ala Glu Thr Ile Glu Ala Leu His Ala Ala Gly Leu Lys Val Trp Val	
660 665 670	
ctc act ggg gac aag atg gag aca gct aaa tcc aca tgc tat gcc tgc	2064
Leu Thr Gly Asp Lys Met Glu Thr Ala Lys Ser Thr Cys Tyr Ala Cys	
675 680 685	
cgc ctt ttc cag acc aac act gag ctc tta gaa cta acc aca aaa acc	2112
Arg Leu Phe Gln Thr Asn Thr Glu Leu Leu Glu Leu Thr Thr Lys Thr	
690 695 700	
att gaa gaa agt gaa agg aaa gaa gat cga tta cat gaa tta ttg ata	2160
Ile Glu Glu Ser Glu Arg Lys Glu Asp Arg Leu His Glu Leu Leu Ile	
705 710 715 720	
gaa tat cgc aag aaa ttg ctg cat gag ttt cct aaa agt act aga agc	2208
Glu Tyr Arg Lys Lys Leu Leu His Glu Phe Pro Lys Ser Thr Arg Ser	
725 730 735	
ttt aaa aaa gca tgg aca gaa cat cag gaa tat gga tta atc ata gat	2256
Phe Lys Lys Ala Trp Thr Glu His Gln Glu Tyr Gly Leu Ile Ile Asp	
740 745 750	
ggc tcc aca ttg tca ctc ata cta aat tct agt caa gac tct agt tca	2304
Gly Ser Thr Leu Ser Leu Ile Leu Asn Ser Ser Gln Asp Ser Ser Ser	
755 760 765	
aac aat tac aaa agc att ttc cta caa ata tgt atg aag tgt act gca	2352

1632
1680
1728
1776
1824
1872
1920
1968
2016
2064
2112
2160
2208
2256
2304
2352


```

1010          1015          1020
gtg att tgg ggt tct tta gcc ttc tat gta ttt ttc tca ttc ttc tgg 3120
Val Ile Trp Gly Ser Leu Ala Phe Tyr Val Phe Phe Ser Phe Phe Trp
1025          1030          1035          1040

gga gga att att tgg cct ttt ctc aag caa cag aga atg tat ttt gta 3168
Gly Gly Ile Ile Trp Pro Phe Leu Lys Gln Gln Arg Met Tyr Phe Val
1045          1050          1055

ttt gcc caa atg ctg tct tct gta tcc aca tgg ttg gct ata att ctt 3216
Phe Ala Gln Met Leu Ser Ser Val Ser Thr Trp Leu Ala Ile Ile Leu
1060          1065          1070

cta ata ttt atc agc ctg ttc cct gag att ctt ctg ata gta tta aag 3264
Leu Ile Phe Ile Ser Leu Phe Pro Glu Ile Leu Leu Ile Val Leu Lys
1075          1080          1085

aat gta aga aga aga agt gcc agg aga aat ctg agc tgt aga agg gca 3312
Asn Val Arg Arg Arg Ser Ala Arg Arg Asn Leu Ser Cys Arg Arg Ala
1090          1095          1100

tct gac tca tta tcc gcc aga cct tca gtc aga cct ctt ctt tta cga 3360
Ser Asp Ser Leu Ser Ala Arg Pro Ser Val Arg Pro Leu Leu Leu Arg
1105          1110          1115          1120

aca ttc tca gac gaa tct aat gta ttg taa 3390
Thr Phe Ser Asp Glu Ser Asn Val Leu *
1125

<210> 16
<211> 6073
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (273)...(4553)

<400> 16
ccacgcgtcc gggaggagcg gagggagaag taggttgcca gctcagcaca ggctccggcg 60
ctggctcccg cagctgagtt tgggagatgt ctaagtgatt tttttttttc ccggaaggca 120
aatggctggc gtggaagcac aaccgcgttt cactcttcga atttgtgctt agctcttttc 180
ttgtaccttg cgactcgtga ccaacatgct gtgatgtgtg ccgagggagg aattggtcag 240
ctacacaacc tggatcttac cacagtttgg at atg act gag gct ctc caa tgg 293
Met Thr Glu Ala Leu Gln Trp
1 5

gcc aga tat cac tgg cga cgg ctg atc aga ggt gca acc agg gat gat 341
Ala Arg Tyr His Trp Arg Arg Leu Ile Arg Gly Ala Thr Arg Asp Asp
10 15 20

gat tca ggg cca tac aac tat tcc tcg ttg ctc gcc tgt ggg cgc aag 389
Asp Ser Gly Pro Tyr Asn Tyr Ser Ser Leu Leu Ala Cys Gly Arg Lys
25 30 35

tcc tct cag atc cct aaa ctg tca gga agg cac cgg att gtt gtt ccc 437
Ser Ser Gln Ile Pro Lys Leu Ser Gly Arg His Arg Ile Val Val Pro
40 45 50 55

```

1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125

His	Glu	Thr	Lys	Ala	Met	Leu	Asn	Asn	Ser	Gly	Pro	Arg	Tyr	Lys	Arg		
				300					305					310			
agc	aaa	tta	gaa	aga	aga	gca	aac	aca	gat	gtc	ctc	tgg	tgt	gtc	atg	1253	
Ser	Lys	Leu	Glu	Arg	Arg	Ala	Asn	Thr	Asp	Val	Leu	Trp	Cys	Val	Met		
			315					320					325				
ctt	ctg	gtc	ata	atg	tgc	tta	act	ggc	gca	gta	ggg	cat	gga	atc	tgg	1301	
Leu	Leu	Val	Ile	Met	Cys	Leu	Thr	Gly	Ala	Val	Gly	His	Gly	Ile	Trp		
		330					335					340					
ctg	agc	agg	tat	gaa	aag	atg	cat	ttt	ttc	aat	gtt	ccc	gag	cct	gat	1349	
Leu	Ser	Arg	Tyr	Glu	Lys	Met	His	Phe	Phe	Asn	Val	Pro	Glu	Pro	Asp		
	345					350					355						
gga	cat	atc	ata	tca	cca	ctg	ttg	gca	gga	ttt	tat	atg	ttt	tgg	acc	1397	
Gly	His	Ile	Ile	Ser	Pro	Leu	Leu	Ala	Gly	Phe	Tyr	Met	Phe	Trp	Thr		
360					365				370						375		
atg	atc	att	ttg	tta	cag	gtc	ttg	att	cct	att	tct	ctc	tat	gtt	tcc	1445	
Met	Ile	Ile	Leu	Leu	Gln	Val	Leu	Ile	Pro	Ile	Ser	Leu	Tyr	Val	Ser		
				380					385					390			
atc	gaa	att	gtg	aag	ctt	gga	caa	ata	tat	ttc	att	caa	agt	gat	gtg	1493	
Ile	Glu	Ile	Val	Lys	Leu	Gly	Gln	Ile	Tyr	Phe	Ile	Gln	Ser	Asp	Val		
			395					400					405				
gat	ttc	tac	aat	gaa	aaa	atg	gat	tct	att	gtt	cag	tgc	cga	gcc	ctg	1541	
Asp	Phe	Tyr	Asn	Glu	Lys	Met	Asp	Ser	Ile	Val	Gln	Cys	Arg	Ala	Leu		
		410					415					420					
aac	atc	gcc	gag	gat	ctg	gga	cag	att	cag	tac	ctc	ttt	tcc	gat	aag	1589	
Asn	Ile	Ala	Glu	Asp	Leu	Gly	Gln	Ile	Gln	Tyr	Leu	Phe	Ser	Asp	Lys		
	425					430					435						
aca	gga	acc	ctc	act	gag	aat	aag	atg	gtt	ttt	cga	aga	tgt	agt	gtg	1637	
Thr	Gly	Thr	Leu	Thr	Glu	Asn	Lys	Met	Val	Phe	Arg	Arg	Cys	Ser	Val		
440					445				450						455		
gca	gga	ttt	gat	tac	tgc	cat	gaa	gaa	aat	gcc	agg	agg	ttg	gag	tcc	1685	
Ala	Gly	Phe	Asp	Tyr	Cys	His	Glu	Glu	Asn	Ala	Arg	Arg	Leu	Glu	Ser		
				460					465					470			
tat	cag	gaa	gct	gtc	tct	gaa	gat	gaa	gat	ttt	ata	gac	aca	gtc	agt	1733	
Tyr	Gln	Glu	Ala	Val	Ser	Glu	Asp	Glu	Asp	Phe	Ile	Asp	Thr	Val	Ser		
			475					480					485				
ggg	tcc	ctc	agc	aat	atg	gca	aaa	cag	aga	gcc	ccc	agc	tgc	agg	aca	1781	
Gly	Ser	Leu	Ser	Asn	Met	Ala	Lys	Pro	Arg	Ala	Pro	Ser	Cys	Arg	Thr		
		490					495					500					
gtt	cat	aat	ggg	cct	ttg	gga	aat	aag	ccc	tca	aat	cat	ctt	gct	ggg	1829	
Val	His	Asn	Gly	Pro	Leu	Gly	Asn	Lys	Pro	Ser	Asn	His	Leu	Ala	Gly		
	505					510					515						
agc	tct	ttt	act	cta	gga	agt	gga	gaa	gga	gcc	agt	gaa	gtg	cct	cat	1877	
Ser	Ser	Phe	Thr	Leu	Gly	Ser	Gly	Glu	Gly	Ala	Ser	Glu	Val	Pro	His		
520					525					530					535		
tcc	aga	cag	gct	gct	ttc	agt	agc	ccc	att	gaa	aca	gac	gtg	gta	cca	1925	
Ser	Arg	Gln	Ala	Ala	Phe	Ser	Ser	Pro	Ile	Glu	Thr	Asp	Val	Val	Pro		

TO THE "EAGLE"

540	545	550	
gac acc agg ctt tta gac aaa ttt agt cag att aca cct cgg ctc ttt Asp Thr Arg Leu Leu Asp Lys Phe Ser Gln Ile Thr Pro Arg Leu Phe 555 560 565			1973
atg cca cta gat gag acc atc caa aat cca cca atg gaa act ttg tac Met Pro Leu Asp Glu Thr Ile Gln Asn Pro Pro Met Glu Thr Leu Tyr 570 575 580			2021
att atc gac ttt ttc att gca ttg gca att tgc aac aca gta gtg gtt Ile Ile Asp Phe Phe Ile Ala Leu Ala Ile Cys Asn Thr Val Val Val 585 590 595			2069
tct gct cct aac caa ccc cga caa aag atc aga cac cct tca ctg ggg Ser Ala Pro Asn Gln Pro Arg Gln Lys Ile Arg His Pro Ser Leu Gly 600 605 610 615			2117
ggg ttg ccc att aag tct ttg gaa gag att aaa agt ctt ttc cag aga Gly Leu Pro Ile Lys Ser Leu Glu Glu Ile Lys Ser Leu Phe Gln Arg 620 625 630			2165
tgg tct gtc cga aga tca agt tct cca tcg ctt aac agt ggg aaa gag Trp Ser Val Arg Arg Ser Ser Ser Pro Ser Leu Asn Ser Gly Lys Glu 635 640 645			2213
cca tct tct gga gtt cca aac gcc ttt gtg agc aga ctc cct ctc ttt Pro Ser Ser Gly Val Pro Asn Ala Phe Val Ser Arg Leu Pro Leu Phe 650 655 660			2261
agt cga atg aaa cca gct tca cct gtg gag gaa gag gtc tcc cag gtg Ser Arg Met Lys Pro Ala Ser Pro Val Glu Glu Glu Val Ser Gln Val 665 670 675			2309
tgt gag agc ccc cag tgc tcc agt agc tca gct tgc tgc aca gaa aca Cys Glu Ser Pro Gln Cys Ser Ser Ser Ser Ala Cys Cys Thr Glu Thr 680 685 690 695			2357
gag aaa caa cac ggt gat gca ggc ctc ctg aat ggc aag gca gag tcc Glu Lys Gln His Gly Asp Ala Gly Leu Leu Asn Gly Lys Ala Glu Ser 700 705 710			2405
ctc cct gga cag cca ttg gcc tgc aac ctg tgt tat gag gcc gag agc Leu Pro Gly Gln Pro Leu Ala Cys Asn Leu Cys Tyr Glu Ala Glu Ser 715 720 725			2453
cca gac gaa gcg gcc tta gtg tat gcc gcc agg gct tac caa tgc act Pro Asp Glu Ala Ala Leu Val Tyr Ala Ala Arg Ala Tyr Gln Cys Thr 730 735 740			2501
tta cgg tct cgg aca cca gag cag gtc atg gtg gac ttt gct gct ttg Leu Arg Ser Arg Thr Pro Glu Gln Val Met Val Asp Phe Ala Ala Leu 745 750 755			2549
gga cca tta aca ttt caa ctc cta cac atc ctg ccc ttt gac tca gta Gly Pro Leu Thr Phe Gln Leu Leu His Ile Leu Pro Phe Asp Ser Val 760 765 770 775			2597
aga aaa aga atg tct gtt gtg gtc cga cac cct ctt tcc aat caa gtt Arg Lys Arg Met Ser Val Val Val Arg His Pro Leu Ser Asn Gln Val 780 785 790			2645

gtg gtg tat acg aaa ggc gct gat tct gtg atc atg gag tta ctg tcg 2693
Val Val Tyr Thr Lys Gly Ala Asp Ser Val Ile Met Glu Leu Leu Ser
795 800 805

gtg gct tcc cca gat gga gca agt ctg gag aaa caa cag atg ata gta 2741
Val Ala Ser Pro Asp Gly Ala Ser Leu Glu Lys Gln Gln Met Ile Val
810 815 820

agg gag aaa acc cag aag cac ttg gat gac tat gcc aaa caa ggc ctt 2789
Arg Glu Lys Thr Gln Lys His Leu Asp Asp Tyr Ala Lys Gln Gly Leu
825 830 835

cgt act tta tgt ata gca aag aag gtc atg agt gac act gaa tat gca 2837
Arg Thr Leu Cys Ile Ala Lys Lys Val Met Ser Asp Thr Glu Tyr Ala
840 845 850 855

gag tgg ctg agg aat cat ttt tta gct gaa acc agc att gac aac agg 2885
Glu Trp Leu Arg Asn His Phe Leu Ala Glu Thr Ser Ile Asp Asn Arg
860 865 870

gaa gaa tta cta ctt gaa tct gcc atg agg ttg gag aac aaa ctt aca 2933
Glu Glu Leu Leu Leu Glu Ser Ala Met Arg Leu Glu Asn Lys Leu Thr
875 880 885

tta ctt ggt gct act ggc att gaa gac cgt ctg cag gag gga gtc cct 2981
Leu Leu Gly Ala Thr Gly Ile Glu Asp Arg Leu Gln Glu Gly Val Pro
890 895 900

gaa tct ata gaa gct ctt cac aaa gcg ggc atc aag atc tgg atg ctg 3029
Glu Ser Ile Glu Ala Leu His Lys Ala Gly Ile Lys Ile Trp Met Leu
905 910 915

aca ggg gac aag cag gag aca gct gtc aac ata gct tat gca tgc aaa 3077
Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Ala Tyr Ala Cys Lys
920 925 930 935

cta ctg gag cca gat gac aag ctt ttt atc ctc aat acc caa agt aaa 3125
Leu Leu Glu Pro Asp Asp Lys Leu Phe Ile Leu Asn Thr Gln Ser Lys
940 945 950

gat gcc tgt ggg atg ctg atg agc aca att ttg aaa gaa ctt cag aag 3173
Asp Ala Cys Gly Met Leu Met Ser Thr Ile Leu Lys Glu Leu Gln Lys
955 960 965

aaa act caa gcc ctg cca gag caa gtg tca tta agt gaa gat tta ctt 3221
Lys Thr Gln Ala Leu Pro Glu Gln Val Ser Leu Ser Glu Asp Leu Leu
970 975 980

cag cct cct gtc ccc cgg gac tca ggg tta cga gct gga ctc att atc 3269
Gln Pro Pro Val Pro Arg Asp Ser Gly Leu Arg Ala Gly Leu Ile Ile
985 990 995

act ggg aag acc ctg gag ttt gcc ctg caa gaa agt ctg caa aag cag 3317
Thr Gly Lys Thr Leu Glu Phe Ala Leu Gln Glu Ser Leu Gln Lys Gln
1000 1005 1010 1015

ttc ctg gaa ctg aca tct tgg tgt caa gct gtg gtc tgc tgc cga gcc 3365
Phe Leu Glu Leu Thr Ser Trp Cys Gln Ala Val Val Cys Cys Arg Ala
1020 1025 1030

T344634001

aca ccg ctg cag aaa agt gaa gtg gtg aaa ttg gtc cgc agc cat ctc 3413
 Thr Pro Leu Gln Lys Ser Glu Val Val Lys Leu Val Arg Ser His Leu
 1035 1040 1045
 cag gtg atg acc ctt gct att ggt gat ggt gcc aat gat gtt agc atg 3461
 Gln Val Met Thr Leu Ala Ile Gly Asp Gly Ala Asn Asp Val Ser Met
 1050 1055 1060
 ata caa gtg gca gac att ggg ata ggg gtc tca ggt caa gaa ggc atg 3509
 Ile Gln Val Ala Asp Ile Gly Ile Gly Val Ser Gly Gln Glu Gly Met
 1065 1070 1075
 cag gct gtg atg gcc agt gac ttt gcc gtt tct cag ttc aaa cat ctc 3557
 Gln Ala Val Met Ala Ser Asp Phe Ala Val Ser Gln Phe Lys His Leu
 1080 1085 1090 1095
 agc aag ctc ctt ctt gtc cat gga cac tgg tgt tat aca cgg ctt tcc 3605
 Ser Lys Leu Leu Leu Val His Gly His Trp Cys Tyr Thr Arg Leu Ser
 1100 1105 1110
 aac atg att ctc tat ttt ttc tat aag aat gtg gcc tat gtg aac ctc 3653
 Asn Met Ile Leu Tyr Phe Phe Tyr Lys Asn Val Ala Tyr Val Asn Leu
 1115 1120 1125
 ctt ttc tgg tac cag ttc ttt tgt gga ttt tca gga aca tcc atg act 3701
 Leu Phe Trp Tyr Gln Phe Phe Cys Gly Phe Ser Gly Thr Ser Met Thr
 1130 1135 1140
 gat tac tgg gtt ttg atc ttc ttc aac ctc ctc ttc aca tct gcc cct 3749
 Asp Tyr Trp Val Leu Ile Phe Phe Asn Leu Leu Phe Thr Ser Ala Pro
 1145 1150 1155
 cct gtc att tat ggt gtt ttg gag aaa gat gtg tct gca gag acc ctc 3797
 Pro Val Ile Tyr Gly Val Leu Glu Lys Asp Val Ser Ala Glu Thr Leu
 1160 1165 1170 1175
 atg caa ctg cct gaa ctt tac aga agt ggt cag aaa tca gag gca tac 3845
 Met Gln Leu Pro Glu Leu Tyr Arg Ser Gly Gln Lys Ser Glu Ala Tyr
 1180 1185 1190
 tta ccc cat acc ttc tgg atc acc tta ttg gat gct ttt tat caa agc 3893
 Leu Pro His Thr Phe Trp Ile Thr Leu Leu Asp Ala Phe Tyr Gln Ser
 1195 1200 1205
 ctg gtc tgc ttc ttt gtg cct tat ttt acc tac cag ggc tca gat act 3941
 Leu Val Cys Phe Phe Val Pro Tyr Phe Thr Tyr Gln Gly Ser Asp Thr
 1210 1215 1220
 gac atc ttt gca ttt gga aac ccc ctg aac aca gcc gct ctg ttc atc 3989
 Asp Ile Phe Ala Phe Gly Asn Pro Leu Asn Thr Ala Ala Leu Phe Ile
 1225 1230 1235
 gtt ctc ctc cat ctg gtc att gaa agc aag agt ttg act tgg att cac 4037
 Val Leu Leu His Leu Val Ile Glu Ser Lys Ser Leu Thr Trp Ile His
 1240 1245 1250 1255
 ttg ctg gtc atc att ggt agc atc ttg tct tat ttt tta ttt gcc ata 4085
 Leu Leu Val Ile Ile Gly Ser Ile Leu Ser Tyr Phe Leu Phe Ala Ile
 1260 1265 1270
 gtt ttt gga gcc atg tgt gta act tgc aac cca cca tcc aac cct tac 4133

1035 1040 1045
 1050 1055 1060
 1065 1070 1075
 1080 1085 1090 1095
 1100 1105 1110
 1115 1120 1125
 1130 1135 1140
 1145 1150 1155
 1160 1165 1170 1175
 1180 1185 1190
 1195 1200 1205
 1210 1215 1220
 1225 1230 1235
 1240 1245 1250 1255
 1260 1265 1270


```

cttctgccta ctattttggt ctgacatttt tgtagccttc tgttattatt ggaaatagtc 5943
tettacataa gctgatttcg agaactttca aaatctcaca tagctaattgg aagttgcttt 6003
ctgctttctt atgactgttt ttataaataa actgtttcat aaataaaaaa aaaaaaaaaa 6063
gggcggccgc                                     6073

```

<210> 17
 <211> 1426
 <212> PRT
 <213> Homo sapiens

<400> 17

Met	Thr	Glu	Ala	Leu	Gln	Trp	Ala	Arg	Tyr	His	Trp	Arg	Arg	Leu	Ile
1				5					10					15	
Arg	Gly	Ala	Thr	Arg	Asp	Asp	Asp	Ser	Gly	Pro	Tyr	Asn	Tyr	Ser	Ser
			20					25				30			
Leu	Leu	Ala	Cys	Gly	Arg	Lys	Ser	Ser	Gln	Ile	Pro	Lys	Leu	Ser	Gly
		35					40					45			
Arg	His	Arg	Ile	Val	Val	Pro	His	Ile	Gln	Pro	Phe	Lys	Asp	Glu	Tyr
	50					55					60				
Glu	Lys	Phe	Ser	Gly	Ala	Tyr	Val	Asn	Asn	Arg	Ile	Arg	Thr	Thr	Lys
65				70				75						80	
Tyr	Thr	Leu	Leu	Asn	Phe	Val	Pro	Arg	Asn	Leu	Phe	Glu	Gln	Phe	His
			85					90					95		
Arg	Ala	Ala	Ser	Leu	Tyr	Phe	Leu	Phe	Leu	Val	Val	Leu	Asn	Trp	Val
			100					105					110		
Pro	Leu	Val	Glu	Ala	Phe	Gln	Lys	Glu	Ile	Thr	Met	Leu	Pro	Leu	Val
		115					120					125			
Val	Val	Leu	Thr	Ile	Ile	Ala	Ile	Lys	Asp	Gly	Leu	Glu	Asp	Tyr	Arg
	130					135					140				
Lys	Tyr	Lys	Ile	Asp	Lys	Gln	Ile	Asn	Asn	Leu	Ile	Thr	Lys	Val	Tyr
145				150				155						160	
Ser	Arg	Lys	Glu	Lys	Lys	Tyr	Ile	Asp	Arg	Cys	Trp	Lys	Asp	Val	Thr
			165					170						175	
Val	Gly	Asp	Phe	Ile	Arg	Leu	Ser	Cys	Asn	Glu	Val	Ile	Pro	Ala	Asp
		180						185					190		
Met	Val	Leu	Leu	Phe	Ser	Thr	Asp	Pro	Asp	Gly	Ile	Cys	His	Ile	Glu
	195						200					205			
Thr	Ser	Gly	Leu	Asp	Gly	Glu	Ser	Asn	Leu	Lys	Gln	Arg	Gln	Val	Val
	210					215					220				
Arg	Gly	Tyr	Ala	Glu	Gln	Asp	Ser	Glu	Val	Asp	Pro	Glu	Lys	Phe	Ser
225					230					235				240	
Ser	Arg	Ile	Glu	Cys	Glu	Ser	Pro	Asn	Asn	Asp	Leu	Ser	Arg	Phe	Arg
			245					250						255	
Gly	Phe	Leu	Glu	His	Ser	Asn	Lys	Glu	Arg	Val	Gly	Leu	Ser	Lys	Glu
		260						265					270		
Asn	Leu	Leu	Leu	Arg	Gly	Cys	Thr	Ile	Arg	Asn	Thr	Glu	Ala	Val	Val
	275						280					285			
Gly	Ile	Val	Val	Tyr	Ala	Gly	His	Glu	Thr	Lys	Ala	Met	Leu	Asn	Asn
	290					295					300				
Ser	Gly	Pro	Arg	Tyr	Lys	Arg	Ser	Lys	Leu	Glu	Arg	Arg	Ala	Asn	Thr
305					310					315				320	
Asp	Val	Leu	Trp	Cys	Val	Met	Leu	Leu	Val	Ile	Met	Cys	Leu	Thr	Gly
			325					330						335	
Ala	Val	Gly	His	Gly	Ile	Trp	Leu	Ser	Arg	Tyr	Glu	Lys	Met	His	Phe
		340					345						350		
Phe	Asn	Val	Pro	Glu	Pro	Asp	Gly	His	Ile	Ile	Ser	Pro	Leu	Leu	Ala
	355						360					365			
Gly	Phe	Tyr	Met	Phe	Trp	Thr	Met	Ile	Ile	Leu	Leu	Gln	Val	Leu	Ile
	370					375					380				
Pro	Ile	Ser	Leu	Tyr	Val	Ser	Ile	Glu	Ile	Val	Lys	Leu	Gly	Gln	Ile
385					390					395				400	

F00432

Tyr	Phe	Ile	Gln	Ser	Asp	Val	Asp	Phe	Tyr	Asn	Glu	Lys	Met	Asp	Ser
				405					410					415	
Ile	Val	Gln	Cys	Arg	Ala	Leu	Asn	Ile	Ala	Glu	Asp	Leu	Gly	Gln	Ile
			420					425					430		
Gln	Tyr	Leu	Phe	Ser	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Glu	Asn	Lys	Met
		435					440					445			
Val	Phe	Arg	Arg	Cys	Ser	Val	Ala	Gly	Phe	Asp	Tyr	Cys	His	Glu	Glu
	450					455					460				
Asn	Ala	Arg	Arg	Leu	Glu	Ser	Tyr	Gln	Glu	Ala	Val	Ser	Glu	Asp	Glu
465				470						475					480
Asp	Phe	Ile	Asp	Thr	Val	Ser	Gly	Ser	Leu	Ser	Asn	Met	Ala	Lys	Pro
			485					490					495		
Arg	Ala	Pro	Ser	Cys	Arg	Thr	Val	His	Asn	Gly	Pro	Leu	Gly	Asn	Lys
			500					505				510			
Pro	Ser	Asn	His	Leu	Ala	Gly	Ser	Ser	Phe	Thr	Leu	Gly	Ser	Gly	Glu
		515					520					525			
Gly	Ala	Ser	Glu	Val	Pro	His	Ser	Arg	Gln	Ala	Ala	Phe	Ser	Ser	Pro
	530					535				540					
Ile	Glu	Thr	Asp	Val	Val	Pro	Asp	Thr	Arg	Leu	Leu	Asp	Lys	Phe	Ser
545				550						555					560
Gln	Ile	Thr	Pro	Arg	Leu	Phe	Met	Pro	Leu	Asp	Glu	Thr	Ile	Gln	Asn
			565					570					575		
Pro	Pro	Met	Glu	Thr	Leu	Tyr	Ile	Ile	Asp	Phe	Phe	Ile	Ala	Leu	Ala
			580					585					590		
Ile	Cys	Asn	Thr	Val	Val	Val	Ser	Ala	Pro	Asn	Gln	Pro	Arg	Gln	Lys
		595					600					605			
Ile	Arg	His	Pro	Ser	Leu	Gly	Gly	Leu	Pro	Ile	Lys	Ser	Leu	Glu	Glu
	610					615					620				
Ile	Lys	Ser	Leu	Phe	Gln	Arg	Trp	Ser	Val	Arg	Arg	Ser	Ser	Ser	Pro
625				630						635					640
Ser	Leu	Asn	Ser	Gly	Lys	Glu	Pro	Ser	Ser	Gly	Val	Pro	Asn	Ala	Phe
			645						650					655	
Val	Ser	Arg	Leu	Pro	Leu	Phe	Ser	Arg	Met	Lys	Pro	Ala	Ser	Pro	Val
			660					665				670			
Glu	Glu	Glu	Val	Ser	Gln	Val	Cys	Glu	Ser	Pro	Gln	Cys	Ser	Ser	Ser
		675					680					685			
Ser	Ala	Cys	Cys	Thr	Glu	Thr	Glu	Lys	Gln	His	Gly	Asp	Ala	Gly	Leu
	690					695					700				
Leu	Asn	Gly	Lys	Ala	Glu	Ser	Leu	Pro	Gly	Gln	Pro	Leu	Ala	Cys	Asn
705				710						715					720
Leu	Cys	Tyr	Glu	Ala	Glu	Ser	Pro	Asp	Glu	Ala	Ala	Leu	Val	Tyr	Ala
			725					730						735	
Ala	Arg	Ala	Tyr	Gln	Cys	Thr	Leu	Arg	Ser	Arg	Thr	Pro	Glu	Gln	Val
		740						745					750		
Met	Val	Asp	Phe	Ala											

					885					890					895
Arg	Leu	Gln	Glu	Gly	Val	Pro	Glu	Ser	Ile	Glu	Ala	Leu	His	Lys	Ala
			900					905					910		
Gly	Ile	Lys	Ile	Trp	Met	Leu	Thr	Gly	Asp	Lys	Gln	Glu	Thr	Ala	Val
		915					920					925			
Asn	Ile	Ala	Tyr	Ala	Cys	Lys	Leu	Leu	Glu	Pro	Asp	Asp	Lys	Leu	Phe
		930				935					940				
Ile	Leu	Asn	Thr	Gln	Ser	Lys	Asp	Ala	Cys	Gly	Met	Leu	Met	Ser	Thr
945					950					955					960
Ile	Leu	Lys	Glu	Leu	Gln	Lys	Lys	Thr	Gln	Ala	Leu	Pro	Glu	Gln	Val
			965						970					975	
Ser	Leu	Ser	Glu	Asp	Leu	Leu	Gln	Pro	Pro	Val	Pro	Arg	Asp	Ser	Gly
			980					985					990		
Leu	Arg	Ala	Gly	Leu	Ile	Ile	Thr	Gly	Lys	Thr	Leu	Glu	Phe	Ala	Leu
		995					1000					1005			
Gln	Glu	Ser	Leu	Gln	Lys	Gln	Phe	Leu	Glu	Leu	Thr	Ser	Trp	Cys	Gln
	1010					1015					1020				
Ala	Val	Val	Cys	Cys	Arg	Ala	Thr	Pro	Leu	Gln	Lys	Ser	Glu	Val	Val
1025					1030					1035					1040
Lys	Leu	Val	Arg	Ser	His	Leu	Gln	Val	Met	Thr	Leu	Ala	Ile	Gly	Asp
				1045					1050					1055	
Gly	Ala	Asn	Asp	Val	Ser	Met	Ile	Gln	Val	Ala	Asp	Ile	Gly	Ile	Gly
		1060						1065					1070		
Val	Ser	Gly	Gln	Glu	Gly	Met	Gln	Ala	Val	Met	Ala	Ser	Asp	Phe	Ala
		1075					1080					1085			
Val	Ser	Gln	Phe	Lys	His	Leu	Ser	Lys	Leu	Leu	Leu	Val	His	Gly	His
	1090					1095					1100				
Trp	Cys	Tyr	Thr	Arg	Leu	Ser	Asn	Met	Ile	Leu	Tyr	Phe	Phe	Tyr	Lys
1105					1110					1115					1120
Asn	Val	Ala	Tyr	Val	Asn	Leu	Leu	Phe	Trp	Tyr	Gln	Phe	Phe	Cys	Gly
				1125					1130					1135	
Phe	Ser	Gly	Thr	Ser	Met	Thr	Asp	Tyr	Trp	Val	Leu	Ile	Phe	Phe	Asn
			1140					1145					1150		
Leu	Leu	Phe	Thr	Ser	Ala	Pro	Pro	Val	Ile	Tyr	Gly	Val	Leu	Glu	Lys
		1155					1160					1165			
Asp	Val	Ser	Ala	Glu	Thr	Leu	Met	Gln	Leu	Pro	Glu	Leu	Tyr	Arg	Ser
	1170					1175					1180				
Gly	Gln	Lys	Ser	Glu	Ala	Tyr	Leu	Pro	His	Thr	Phe	Trp	Ile	Thr	Leu
1185					1190					1195					1200
Leu	Asp	Ala	Phe	Tyr	Gln	Ser	Leu	Val	Cys	Phe	Phe	Val	Pro	Tyr	Phe
				1205					1210					1215	
Thr	Tyr	Gln	Gly	Ser	Asp	Thr	Asp	Ile	Phe	Ala	Phe	Gly	Asn	Pro	Leu
			1220					1225					1230		
Asn	Thr	Ala	Ala	Leu	Phe	Ile	Val	Leu	Leu	His					

Pro Gly Pro Ser Ala Val Phe Ala Met Lys Ser Ala Thr Ser Cys Ala
 1380 1385 1390
 Ile Glu Gln Gly Asn Leu Ser Leu Cys Glu Thr Ala Leu Asp Gln Gly
 1395 1400 1405
 Tyr Ser Glu Thr Lys Ala Phe Glu Met Ala Gly Pro Ser Lys Gly Lys
 1410 1415 1420
 Glu Ser
 1425

<210> 18
 <211> 4281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(4281)

<400> 18
 atg act gag gct ctc caa tgg gcc aga tat cac tgg cga cgg ctg atc 48
 Met Thr Glu Ala Leu Gln Trp Ala Arg Tyr His Trp Arg Arg Leu Ile
 1 5 10 15
 aga ggt gca acc agg gat gat gat tca ggg cca tac aac tat tcc tcg 96
 Arg Gly Ala Thr Arg Asp Asp Asp Ser Gly Pro Tyr Asn Tyr Ser Ser
 20 25 30
 ttg ctc gcc tgt ggg cgc aag tcc tct cag atc cct aaa ctg tca gga 144
 Leu Leu Ala Cys Gly Arg Lys Ser Ser Gln Ile Pro Lys Leu Ser Gly
 35 40 45
 agg cac cgg att gtt gtt ccc cac atc cag ccc ttc aag gat gag tat 192
 Arg His Arg Ile Val Val Pro His Ile Gln Pro Phe Lys Asp Glu Tyr
 50 55 60
 gag aag ttc tcc gga gcc tat gtg aac aat cga ata cga aca aca aag 240
 Glu Lys Phe Ser Gly Ala Tyr Val Asn Asn Arg Ile Arg Thr Thr Lys
 65 70 75 80
 tac aca ctt ctg aat ttt gtg cca aga aat tta ttt gaa caa ttt cac 288
 Tyr Thr Leu Leu Asn Phe Val Pro Arg Asn Leu Phe Glu Gln Phe His
 85 90 95
 aga gct gcc agt tta tat ttc ctg ttc cta gtt gtc ctg aac tgg gta 336
 Arg Ala Ala Ser Leu Tyr Phe Leu Phe Leu Val Val Leu Asn Trp Val
 100 105 110
 cct ttg gta gaa gcc ttc caa aag gaa atc acc atg ttg cct ctg gtg 384
 Pro Leu Val Glu Ala Phe Gln Lys Glu Ile Thr Met Leu Pro Leu Val
 115 120 125
 gtg gtc ctt aca att atc gca att aaa gat ggc ctg gaa gat tat cgg 432
 Val Val Leu Thr Ile Ile Ala Ile Lys Asp Gly Leu Glu Asp Tyr Arg
 130 135 140
 aaa tac aaa att gac aaa cag atc aat aat tta ata act aaa gtt tat 480
 Lys Tyr Lys Ile Asp Lys Gln Ile Asn Asn Leu Ile Thr Lys Val Tyr
 145 150 155 160
 agt agg aaa gag aaa aaa tac att gac cga tgc tgg aaa gac gtt act 528

100463 100463

gtg agc aga ctc cct ctc ttt agt cga atg aaa cca gct tca cct gtg	2016
Val Ser Arg Leu Pro Leu Phe Ser Arg Met Lys Pro Ala Ser Pro Val	
660 665 670	
gag gaa gag gtc tcc cag gtg tgt gag agc ccc cag tgc tcc agt agc	2064
Glu Glu Glu Val Ser Gln Val Cys Glu Ser Pro Gln Cys Ser Ser Ser	
675 680 685	
tca gct tgc tgc aca gaa aca gag aaa caa cac ggt gat gca ggc ctc	2112
Ser Ala Cys Cys Thr Glu Thr Glu Lys Gln His Gly Asp Ala Gly Leu	
690 695 700	
ctg aat ggc aag gca gag tcc ctc cct gga cag cca ttg gcc tgc aac	2160
Leu Asn Gly Lys Ala Glu Ser Leu Pro Gly Gln Pro Leu Ala Cys Asn	
705 710 715 720	
ctg tgt tat gag gcc gag agc cca gac gaa gcg gcc tta gtg tat gcc	2208
Leu Cys Tyr Glu Ala Glu Ser Pro Asp Glu Ala Ala Leu Val Tyr Ala	
725 730 735	
gcc agg gct tac caa tgc act tta cgg tct cgg aca cca gag cag gtc	2256
Ala Arg Ala Tyr Gln Cys Thr Leu Arg Ser Arg Thr Pro Glu Gln Val	
740 745 750	
atg gtg gac ttt gct gct ttg gga cca tta aca ttt caa ctc cta cac	2304
Met Val Asp Phe Ala Ala Leu Gly Pro Leu Thr Phe Gln Leu Leu His	
755 760 765	
atc ctg ccc ttt gac tca gta aga aaa aga atg tct gtt gtg gtc cga	2352
Ile Leu Pro Phe Asp Ser Val Arg Lys Arg Met Ser Val Val Val Arg	
770 775 780	
cac cct ctt tcc aat caa gtt gtg gtg tat acg aaa ggc gct gat tct	2400
His Pro Leu Ser Asn Gln Val Val Val Tyr Thr Lys Gly Ala Asp Ser	
785 790 795 800	
gtg atc atg gag tta ctg tcg gtg gct tcc cca gat gga gca agt ctg	2448
Val Ile Met Glu Leu Ser Val Ala Ser Pro Asp Gly Ala Ser Leu	
805 810 815	
gag aaa caa cag atg ata gta agg gag aaa acc cag aag cac ttg gat	2496
Glu Lys Gln Gln Met Ile Val Arg Glu Lys Thr Gln Lys His Leu Asp	
820 825 830	
gac tat gcc aaa caa ggc ctt cgt act tta tgt ata gca aag aag gtc	2544
Asp Tyr Ala Lys Gln Gly Leu Arg Thr Leu Cys Ile Ala Lys Lys Val	
835 840 845	
atg agt gac act gaa tat gca gag tgg ctg agg aat cat ttt tta gct	2592
Met Ser Asp Thr Glu Tyr Ala Glu Trp Leu Arg Asn His Phe Leu Ala	
850 855 860	
gaa acc agc att gac aac agg gaa gaa tta cta ctt gaa tct gcc atg	2640
Glu Thr Ser Ile Asp Asn Arg Glu Glu Leu Leu Leu Glu Ser Ala Met	
865 870 875 880	
agg ttg gag aac aaa ctt aca tta ctt ggt gct act ggc att gaa gac	2688
Arg Leu Glu Asn Lys Leu Thr Leu Leu Gly Ala Thr Gly Ile Glu Asp	
885 890 895	

100453-100454

cgt	ctg	cag	gag	gga	gtc	cct	gaa	tct	ata	gaa	gct	ctt	cac	aaa	gcg	2736
Arg	Leu	Gln	Glu	Gly	Val	Pro	Glu	Ser	Ile	Glu	Ala	Leu	His	Lys	Ala	
			900					905						910		
ggc	atc	aag	atc	tgg	atg	ctg	aca	ggg	gac	aag	cag	gag	aca	gct	gtc	2784
Gly	Ile	Lys	Ile	Trp	Met	Leu	Thr	Gly	Asp	Lys	Gln	Glu	Thr	Ala	Val	
		915					920					925				
aac	ata	gct	tat	gca	tgc	aaa	cta	ctg	gag	cca	gat	gac	aag	ctt	ttt	2832
Asn	Ile	Ala	Tyr	Ala	Cys	Lys	Leu	Leu	Glu	Pro	Asp	Asp	Lys	Leu	Phe	
		930				935					940					
atc	ctc	aat	acc	caa	agt	aaa	gat	gcc	tgt	ggg	atg	ctg	atg	agc	aca	2880
Ile	Leu	Asn	Thr	Gln	Ser	Lys	Asp	Ala	Cys	Gly	Met	Leu	Met	Ser	Thr	
					950					955					960	
att	ttg	aaa	gaa	ctt	cag	aag	aaa	act	caa	gcc	ctg	cca	gag	caa	gtg	2928
Ile	Leu	Lys	Glu	Leu	Gln	Lys	Lys	Thr	Gln	Ala	Leu	Pro	Glu	Gln	Val	
				965					970					975		
tca	tta	agt	gaa	gat	tta	ctt	cag	cct	cct	gtc	ccc	cgg	gac	tca	ggg	2976
Ser	Leu	Ser	Glu	Asp	Leu	Leu	Gln	Pro	Pro	Val	Pro	Arg	Asp	Ser	Gly	
			980					985					990			
tta	cga	gct	gga	ctc	att	atc	act	ggg	aag	acc	ctg	gag	ttt	gcc	ctg	3024
Leu	Arg	Ala	Gly	Leu	Ile	Ile	Thr	Gly	Lys	Thr	Leu	Glu	Phe	Ala	Leu	
		995					1000					1005				
caa	gaa	agt	ctg	caa	aag	cag	ttc	ctg	gaa	ctg	aca	tct	tgg	tgt	caa	3072
Gln	Glu	Ser	Leu	Gln	Lys	Gln	Phe	Leu	Glu	Leu	Thr	Ser	Trp	Cys	Gln	
		1010				1015					1020					
gct	gtg	gtc	tgc	tgc	cga	gcc	aca	cgg	ctg	cag	aaa	agt	gaa	gtg	gtg	3120
Ala	Val	Val	Cys	Cys	Arg	Ala	Thr	Pro	Leu	Gln	Lys	Ser	Glu	Val	Val	
		1025			1030					1035					1040	
aaa	ttg	gtc	cgc	agc	cat	ctc	cag	gtg	atg	acc	ctt	gct	att	ggg	gat	3168
Lys	Leu	Val	Arg	Ser	His	Leu	Gln	Val	Met	Thr	Leu	Ala	Ile	Gly	Asp	
				1045					1050					1055		
ggg	gcc	aat	gat	gtt	agc	atg	ata	caa	gtg	gca	gac	att	ggg	ata	ggg	3216
Gly	Ala	Asn	Asp	Val	Ser	Met	Ile	Gln	Val	Ala	Asp	Ile	Gly	Ile	Gly	
			1060					1065					1070			
gtc	tca	ggg	caa	gaa	ggc	atg	cag	gct	gtg	atg	gcc	agt	gac	ttt	gcc	3264
Val	Ser	Gly	Gln	Glu	Gly	Met	Gln	Ala	Val	Met	Ala	Ser	Asp	Phe	Ala	
		1075					1080				1085					
gtt	tct	cag	ttc	aaa	cat	ctc	agc	aag	ctc	ctt	ctt	gtc	cat	gga	cac	3312
Val	Ser	Gln	Phe	Lys	His	Leu	Ser	Lys	Leu	Leu	Leu	Val	His	Gly	His	
		1090				1095					1100					
tgg	tgt	tat	aca	cgg	ctt	tcc	aac	atg	att	ctc	tat	ttt	ttc	tat	aag	3360
Trp	Cys	Tyr	Thr	Arg	Leu	Ser	Asn	Met	Ile	Leu	Tyr	Phe	Phe	Tyr	Lys	
		1105			1110					1115					1120	
aat	gtg	gcc	tat	gtg	aac	ctc	ctt	ttc	tgg	tac	cag	ttc	ttt	tgt	gga	3408
Asn	Val	Ala	Tyr	Val	Asn	Leu	Leu	Phe	Trp	Tyr	Gln	Phe	Phe	Cys	Gly	
				1125					1130					1135		
ttt	tca	gga	aca	tcc	atg	act	gat	tac	tgg	gtt	ttg	atc	ttc	ttc	aac	3456

100453-4304

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																																
Population (millions)	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4.0	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5	7.6	7.7	7.8	7.9	8.0	8.1	8.2	8.3	8.4	8.5	8.6	8.7	8.8	8.9	9.0	9.1	9.2	9.3	9.4	9.5	9.6	9.7	9.8	9.9	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	50.5 (10.5)
Female	51.5 (11.5)
Marital status	
Married	75.5%
Single	24.5%
Divorced	1.0%
Widowed	0.5%
Education level	
High school or above	85.5%
Below high school	14.5%
Occupation	
Professional	35.5%
Managerial	25.5%
Technical	15.5%
Service	10.5%
Unemployed	12.5%
Retired	1.0%
Income (US\$)	
<1000	15.5%
1000-2000	35.5%
2000-3000	25.5%
>3000	23.5%
Health insurance	
Yes	85.5%
No	14.5%
Smoking status	
Smoker	15.5%
Non-smoker	84.5%
Alcohol consumption	
Yes	10.5%
No	89.5%
Family size	
1-2	45.5%
3-4	35.5%
5-6	15.5%
7-8	2.5%
9-10	1.0%
11-12	0.5%
13-14	0.5%
15-16	0.5%
17-18	0.5%
19-20	0.5%
21-22	0.5%
23-24	0.5%
25-26	0.5%
27-28	0.5%
29-30	0.5%
31-32	0.5%
33-34	0.5%
35-36	0.5%
37-38	0.5%
39-40	0.5%
41-42	0.5%
43-44	0.5%
45-46	0.5%
47-48	0.5%
49-50	0.5%
51-52	0.5%
53-54	0.5%
55-56	0.5%
57-58	0.5%
59-60	0.5%
61-62	0.5%
63-64	0.5%
65-66	0.5%
67-68	0.5%
69-70	0.5%
71-72	0.5%
73-74	0.5%
75-76	0.5%
77-78	0.5%
79-80	0.5%
81-82	0.5%
83-84	0.5%
85-86	0.5%
87-88	0.5%
89-90	0.5%
91-92	0.5%
93-94	0.5%
95-96	0.5%
97-98	0.5%
99-100	0.5%
101-102	0.5%
103-104	0.5%
105-106	0.5%
107-108	0.5%
109-110	0.5%
111-112	0.5%
113-114	0.5%
115-116	0.5%
117-118	0.5%
119-120	0.5%
121-122	0.5%
123-124	0.5%
125-126	0.5%
127-128	0.5%
129-130	0.5%
131-132	0.5%
133-134	0.5%
135-136	0.5%
137-138	0.5%
139-140	0.5%
141-142	0.5%
143-144	0.5%
145-146	0.5%
147-148	0.5%
149-150	0.5%
151-152	0.5%
153-154	0.5%
155-156	0.5%
157-158	0.5%
159-160	0.5%
161-162	0.5%
163-164	0.5%
165-166	0.5%
167-168	0.5%
169-170	0.5%
171-172	0.5%
173-174	0.5%
175-176	0.5%
177-178	0.5%
179-180	0.5%
181-182	0.5%
183-184	0.5%
185-186	0.5%
187-188	0.5%
189-190	0.5%
191-192	0.5%
193-194	0.5%
195-196	0.5%
197-198	0.5%
199-200	0.5%

	120	125	130	
ctt gta aaa act aga tca aaa aac att cgg gtg ggt gat att gtt cga				607
Leu Val Lys Thr Arg Ser Lys Asn Ile Arg Val Gly Asp Ile Val Arg				
	135	140	145	
ata gcc aaa gat gaa att ttt cct gca gac ttg gtg ctt ctg tcc tca				655
Ile Ala Lys Asp Glu Ile Phe Pro Ala Asp Leu Val Leu Leu Ser Ser				
	150	155	160	
gat cga ctg gat ggt tcc tgt cac gtt aca act gct agt ttg gac gga				703
Asp Arg Leu Asp Gly Ser Cys His Val Thr Thr Ala Ser Leu Asp Gly				
	165	170	175	
gaa act aac ctg aag aca cat gtg gca gtt cca gaa aca gca tta tta				751
Glu Thr Asn Leu Lys Thr His Val Ala Val Pro Glu Thr Ala Leu Leu				
	180	185	190	195
caa aca gtt gcc aat ttg gac act cta gta gct gta ata gaa tgc cag				799
Gln Thr Val Ala Asn Leu Asp Thr Leu Val Ala Val Ile Glu Cys Gln				
	200	205	210	
caa cca gaa gca gac tta tac aga ttc atg gga cga atg atc ata acc				847
Gln Pro Glu Ala Asp Leu Tyr Arg Phe Met Gly Arg Met Ile Ile Thr				
	215	220	225	
caa caa atg gaa gaa att gta aga cct ctg ggg ccg gag agt ctc ctg				895
Gln Gln Met Glu Glu Ile Val Arg Pro Leu Gly Pro Glu Ser Leu Leu				
	230	235	240	
ctt cgt gga gcc aga tta aaa aac aca aaa gaa att ttt ggt gtt gcg				943
Leu Arg Gly Ala Arg Leu Lys Asn Thr Lys Glu Ile Phe Gly Val Ala				
	245	250	255	
gta tac act gga atg gaa act aag atg gca tta aat tac aag agc aaa				991
Val Tyr Thr Gly Met Glu Thr Lys Met Ala Leu Asn Tyr Lys Ser Lys				
	260	265	270	275
tca cag aaa cga tct gca gta gaa aag tca atg aat aca ttt ttg ata				1039
Ser Gln Lys Arg Ser Ala Val Glu Lys Ser Met Asn Thr Phe Leu Ile				
	280	285	290	
att tat cta gta att ctt ata tct gaa gct gtc atc agc act atc ttg				1087
Ile Tyr Leu Val Ile Leu Ile Ser Glu Ala Val Ile Ser Thr Ile Leu				
	295	300	305	
aag tat aca tgg caa gct gaa gaa aaa tgg gat gaa cct tgg tat aac				1135
Lys Tyr Thr Trp Gln Ala Glu Glu Lys Trp Asp Glu Pro Trp Tyr Asn				
	310	315	320	
caa aaa aca gaa cat caa aga aat agc agt aag att ctg aga ttt att				1183
Gln Lys Thr Glu His Gln Arg Asn Ser Ser Lys Ile Leu Arg Phe Ile				
	325	330	335	
tca gac ttc ctt gct ttt ttg gtt ctc tac aat ttc atc att cca att				1231
Ser Asp Phe Leu Ala Phe Leu Val Leu Tyr Asn Phe Ile Ile Pro Ile				
	340	345	350	355
tca tta tat gtg aca gtc gaa atg cag aaa ttt ctt gga tca ttt ttt				1279
Ser Leu Tyr Val Thr Val Glu Met Gln Lys Phe Leu Gly Ser Phe Phe				
	360	365	370	

120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370

att ggc tgg gat ctt gat ctg tat cat gaa gaa tca gat cag aaa gct 1327
 Ile Gly Trp Asp Leu Asp Leu Tyr His Glu Glu Ser Asp Gln Lys Ala
 375 380 385

caa gtc aat act tcc gat ctg aat gaa gag ctt gga cag gta gag tac 1375
 Gln Val Asn Thr Ser Asp Leu Asn Glu Glu Leu Gly Gln Val Glu Tyr
 390 395 400

gtg ttt aca gat aaa act ggt aca ctg aca gaa aat gag atg cag ttt 1423
 Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu Asn Glu Met Gln Phe
 405 410 415

cgg gaa tgt tca att aat ggc atg aaa tac caa gaa att aat ggt aga 1471
 Arg Glu Cys Ser Ile Asn Gly Met Lys Tyr Gln Glu Ile Asn Gly Arg
 420 425 430 435

ctt gta ccc gaa gga cca aca cca gac tct tca gaa gga aac tta tct 1519
 Leu Val Pro Glu Gly Pro Thr Pro Asp Ser Ser Glu Gly Asn Leu Ser
 440 445 450

tat ctt agt agt tta tcc cat ctt aac aac tta tcc cat ctt aca acc 1567
 Tyr Leu Ser Ser Leu Ser His Leu Asn Asn Leu Ser His Leu Thr Thr
 455 460 465

agt tcc tct ttc aga acc agt cct gaa aat gaa act gaa cta att aaa 1615
 Ser Ser Ser Phe Arg Thr Ser Pro Glu Asn Glu Thr Glu Leu Ile Lys
 470 475 480

gaa cat gat ctc ttc ttt aaa gca gtc agt ctc tgt cac act gta cag 1663
 Glu His Asp Leu Phe Phe Lys Ala Val Ser Leu Cys His Thr Val Gln
 485 490 495

att agc aat gtt caa act gac tgc act ggt gat ggt ccc tgg caa tcc 1711
 Ile Ser Asn Val Gln Thr Asp Cys Thr Gly Asp Gly Pro Trp Gln Ser
 500 505 510 515

aac ctg gca cca tgc cag ttg gag tac tat gca tct tca cca gat gaa 1759
 Asn Leu Ala Pro Ser Gln Leu Glu Tyr Tyr Ala Ser Ser Pro Asp Glu
 520 525 530

aag gct cta gta gaa gct gct gca agg att ggt att gtg ttt att ggc 1807
 Lys Ala Leu Val Glu Ala Ala Ala Arg Ile Gly Ile Val Phe Ile Gly
 535 540 545

aat tct gaa gaa act atg gag gtt aaa act ctt gga aaa ctg gaa cgg 1855
 Asn Ser Glu Glu Thr Met Glu Val Lys Thr Leu Gly Lys Leu Glu Arg
 550 555 560

tac aaa ctg ctt cat att ctg gaa ttt gat tca gat cgt agg aga atg 1903
 Tyr Lys Leu Leu His Ile Leu Glu Phe Asp Ser Asp Arg Arg Arg Met
 565 570 575

agt gta att gtt cag gca cct tca ggt gag aag tta tta ttt gct aaa 1951
 Ser Val Ile Val Gln Ala Pro Ser Gly Glu Lys Leu Leu Phe Ala Lys
 580 585 590 595

gga gct gag tca tca att ctc cct aaa tgt ata ggt gga gaa ata gaa 1999
 Gly Ala Glu Ser Ser Ile Leu Pro Lys Cys Ile Gly Gly Glu Ile Glu
 600 605 610

T
O
T
A
L
C
O
U
N
T
:
1
0
9
4
9

aaa acc aga att cat gta gat gaa ttt gct ttg aaa ggg cta aga act 2047
 Lys Thr Arg Ile His Val Asp Glu Phe Ala Leu Lys Gly Leu Arg Thr
 615 620 625

ctg tgt ata gca tat aga aaa ttt aca tca aaa gag tat gag gaa ata 2095
 Leu Cys Ile Ala Tyr Arg Lys Phe Thr Ser Lys Glu Tyr Glu Glu Ile
 630 635 640

gat aaa cgc ata ttt gaa gcc agg act gcc ttg cag cag cgg gaa gag 2143
 Asp Lys Arg Ile Phe Glu Ala Arg Thr Ala Leu Gln Gln Arg Glu Glu
 645 650 655

aaa ttg gca gct gtt ttc cag ttc ata gag aaa gac ctg ata tta ctt 2191
 Lys Leu Ala Ala Val Phe Gln Phe Ile Glu Lys Asp Leu Ile Leu Leu
 660 665 670 675

gga gcc aca gca gta gaa gac aga cta caa gat aaa gtt cga gaa act 2239
 Gly Ala Thr Ala Val Glu Asp Arg Leu Gln Asp Lys Val Arg Glu Thr
 680 685 690

att gaa gca ttg aga atg gct ggt atc aaa gta tgg gta ctt act ggg 2287
 Ile Glu Ala Leu Arg Met Ala Gly Ile Lys Val Trp Val Leu Thr Gly
 695 700 705

gat aaa cat gaa aca gct gtt agt gtg agt tta tca tgt ggc cat ttt 2335
 Asp Lys His Glu Thr Ala Val Ser Val Ser Leu Ser Cys Gly His Phe
 710 715 720

cat aga acc atg aac atc ctt gaa ctt ata aac cag aaa tca gac agc 2383
 His Arg Thr Met Asn Ile Leu Glu Leu Ile Asn Gln Lys Ser Asp Ser
 725 730 735

gag tgt gct gaa caa ttg agg cag ctt gcc aga aga att aca gag gat 2431
 Glu Cys Ala Glu Gln Leu Arg Gln Leu Ala Arg Arg Ile Thr Glu Asp
 740 745 750 755

cat gtg att cag cat ggg ctg gta gtg gat ggg acc agc cta tct ctt 2479
 His Val Ile Gln His Gly Leu Val Val Asp Gly Thr Ser Leu Ser Leu
 760 765 770

gca ctc agg gag cat gaa aaa cta ttt atg gaa gtt tgc aga aat tgt 2527
 Ala Leu Arg Glu His Glu Lys Leu Phe Met Glu Val Cys Arg Asn Cys
 775 780 785

tca gct gta tta tgc tgt cgt atg gct cca ctg cag aaa gca aaa gta 2575
 Ser Ala Val Leu Cys Cys Arg Met Ala Pro Leu Gln Lys Ala Lys Val
 790 795 800

ata aga cta ata aaa ata tca cct gag aaa cct ata aca ttg gct gtt 2623
 Ile Arg Leu Ile Lys Ile Ser Pro Glu Lys Pro Ile Thr Leu Ala Val
 805 810 815

ggt gat ggt gct aat gac gta agc atg ata caa gaa gcc cat gtt ggc 2671
 Gly Asp Gly Ala Asn Asp Val Ser Met Ile Gln Glu Ala His Val Gly
 820 825 830 835

ata gga atc atg ggt aaa gaa gga aga cag gct gca aga aac agt gac 2719
 Ile Gly Ile Met Gly Lys Glu Gly Arg Gln Ala Ala Arg Asn Ser Asp
 840 845 850

tat gca ata gcc aga ttt aag ttc ctc tcc aaa ttg ctt ttt gtt cat 2767

Variable	Mean	SD	Min	Max
Age	34.5	10.5	18	65
Gender	50%	50%	Male	Female
Marital status	75%	25%	Married	Single
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Occupation	45%	55%	Professional	Non-professional
Religion	60%	40%	Muslim	Other
Health status	85%	15%	Good	Poor
Smoking status	30%	70%	Smoker	Non-smoker
Alcohol consumption	10%	90%	Drinker	Non-drinker
Exercise frequency	20%	80%	Regular	Irregular
Stress level	65%	35%	Low	High
Sleep quality	70%	30%	Good	Poor
Dietary habits	55%	45%	Healthy	Unhealthy
Family size	3.5	1.5	1	6
Urban/rural	60%	40%	Urban	Rural
Health insurance	80%	20%	Insured	Uninsured
Healthcare access	75%	25%	Easy	Difficult
Healthcare cost	1500	500	500	3000
Healthcare quality	60%	40%	Good	Poor
Healthcare satisfaction	55%	45%	Satisfied	Dissatisfied
Healthcare utilization	70%	30%	High	Low
Healthcare expenditure	10%	90%	Low	High
Healthcare coverage	85%	15%	Covered	Not covered
Healthcare equity	60%	40%	Equal	Unequal
Healthcare transparency	50%	50%	Transparent	Opaque
Healthcare accountability	65%	35%	Accountable	Not accountable
Healthcare integrity	70%	30%	Integrity	No integrity
Healthcare ethics	60%	40%	Ethical	Unethical
Healthcare professionalism	75%	25%	Professional	Unprofessional
Healthcare competence	80%	20%	Competent	Incompetent
Healthcare communication	65%	35%	Good	Poor
Healthcare collaboration	70%	30%	Collaborative	Non-collaborative
Healthcare leadership	60%	40%	Leadership	No leadership
Healthcare innovation	55%	45%	Innovative	Not innovative
Healthcare research	65%	35%	Research	No research
Healthcare education	70%	30%	Educational	Non-educational
Healthcare training	60%	40%	Trained	Not trained
Healthcare certification	75%	25%	Certified	Not certified
Healthcare accreditation	80%	20%	Accredited	Not accredited
Healthcare regulation	65%	35%	Regulated	Not regulated
Healthcare supervision	70%	30%	Supervised	Not supervised
Healthcare monitoring	60%	40%	Monitored	Not monitored
Healthcare evaluation	75%	25%	Evaluated	Not evaluated
Healthcare improvement	80%	20%	Improved	Not improved
Healthcare reform	65%	35%	Reformed	Not reformed
Healthcare development	70%	30%	Developed	Not developed
Healthcare progress	60%	40%	Progress	No progress
Healthcare success	75%	25%	Successful	Unsuccessful
Healthcare failure	25%	75%	Failed	Not failed
Healthcare challenge	60%	40%	Challenged	Not challenged
Healthcare opportunity	70%	30%	Opportunity	No opportunity
Healthcare risk	65%	35%	Risky	Not risky
Healthcare benefit	75%	25%	Beneficial	Not beneficial
Healthcare harm	25%	75%	Harmful	Not harmful
Healthcare impact	60%	40%	Impact	No impact
Healthcare effect	70%	30%	Effective	Not effective
Healthcare result	65%	35%	Result	No result
Healthcare outcome	75%	25%	Outcome	No outcome
Healthcare conclusion	80%	20%	Conclusion	No conclusion
Healthcare recommendation	65%	35%	Recommended	Not recommended
Healthcare suggestion	70%	30%	Suggested	Not suggested
Healthcare advice	60%	40%	Advised	Not advised
Healthcare instruction	75%	25%	Instructed	Not instructed
Healthcare guidance	80%	20%	Guided	Not guided
Healthcare support	65%	35%	Supported	Not supported
Healthcare assistance	70%	30%	Assisted	Not assisted
Healthcare help	60%	40%	Helped	Not helped
Healthcare aid	75%	25%	Aided	Not aided
Healthcare relief	80%	20%	Relieved	Not relieved
Healthcare comfort	65%	35%	Comforted	Not comforted
Healthcare ease	70%	30%	Eased	Not eased
Healthcare convenience	60%	40%	Convenient	Not convenient
Healthcare accessibility	75%	25%	Accessible	Not accessible
Healthcare availability	80%	20%	Available	Not available
Healthcare proximity	65%	35%	Proximate	Not proximate
Healthcare distance	70%	30%	Distant	Not distant
Healthcare location	60%	40%	Located	Not located
Healthcare setting	75%	25%	Setting	No setting
Healthcare environment	80%	20%	Environment	No environment
Healthcare atmosphere	65%	35%	Atmosphere	No atmosphere
Healthcare mood	70%	30%	Mood	No mood
Healthcare tone	60%	40%	Tone	No tone
Healthcare style	75%	25%	Style	No style
Healthcare design	80%	20%	Design	No design
Healthcare layout				

1095	1100	1105	
act gaa aca aat gca ggt atc aag tgc ttg gac tcc atg tgc tgt ttc			3535
Thr Glu Thr Asn Ala Gly Ile Lys Cys Leu Asp Ser Met Cys Cys Phe			
1110	1115	1120	
ccg gaa gga gaa gca gcg tgt gca tct gtt gga aga atg ctg gaa cga			3583
Pro Glu Gly Glu Ala Ala Cys Ala Ser Val Gly Arg Met Leu Glu Arg			
1125	1130	1135	
gtt ata gga aga tgt agt cca acc cac atc agc agt tca tgg agt gca			3631
Val Ile Gly Arg Cys Ser Pro Thr His Ile Ser Ser Ser Trp Ser Ala			
1140	1145	1150	1155
tcg gat cct ttc tat acc aac gac agg agc atc ttg act ctc tcc aca			3679
Ser Asp Pro Phe Tyr Thr Asn Asp Arg Ser Ile Leu Thr Leu Ser Thr			
1160	1165	1170	
atg gac tca tct act tgt taa aggggcagta gtactttgtg ggagccagtt			3730
Met Asp Ser Ser Thr Cys *			
1175			
cacctccttt cctaaaattc agtgtgatca ccctgttaat ggccacacta gctctgaaat			3790
taattttccaa aatcttttcta gtagttcata cccactcaga gttataatgg caaacaaca			3850
gaaagcatta gtacaagccc ctcccaacac ccttaatttg aatctgaaca tgtaaataat			3910
tgagaataaa gagacatttt tcatctcttt gtctgggttg tcccttggtg ttatgggact			3970
cctaattggca tttcagtcgt ttgctgaggc cattatatatt taatataaat gtagaaaaaa			4030
gagagaaatc ttagtaaaaga gtatttttta gtattagctt gattattgac tcttctattt			4090
aaatctgctt ctgtaaaatta tgcgtgaaagt ttgccttgag aactctattt ttttattaga			4150
gttatatttta aagctttttca tgggaaaagt taatgtgaat actgaggaat tttggtccct			4210
cagtgacctg tgttggttaat tcattaatgc attctgagtt cacagagcaa attaggagaa			4270
tcatttccaa ccattatttta ctgcagtagt gggagtaaat ttataccaat tcctctaact			4330
gtactgtaac acagcctgta aagttagcca tataaatgca aggggtatata atataataa			4390
atcaggaatc aggtccgttc accgaacttc aaattgatgt ttactaatat ttttgtgaca			4450
gagtataaag accctatagt gggtaaatga gatactatta gcatattatt aatttaattgt			4510
ctttatcatt ggatcttttg catgctttta tctgggttaac atattttaaat ttgctttttt			4570
tctctttacc tgaaggctct gtgtatagta tttcatgaca tcgttggtaca gtttaactat			4630
caataaaaaag tttggacagt atttaaatat tgcaaatatg ttttaattata caaatcagaa			4690
tagtatgggt aattaaatga atacaaaaag aagagcctct ttctgcagcc gacttagaca			4750
tgctcttccc tttctataag ctgattttta gaataaaggg tttcagttaa taatcttatt			4810
ttcaggttat gtcattctaac ttatagcaaa ctaccacaat acagttaggt ctgccagtgt			4870
cccagtacaa ggcatatttc aggtgtggct gtggaatgta aaaatgctca acttgatatca			4930
ggtaatgtta gcaataaatt aaatgctaag aatgattaat cgggtacatg ttactgtaat			4990
taactcattg cacttcaaaa cctaacttcc atcctgaatt tatcaagtag ttcagtattg			5050
tcatttgttt ttgttttatt gaaaagtaat gttgtcttaa gatttagaag tgattattag			5110
cttgagaact attaccagc tctaagcaaa taatgattgt atacatatta agataatgg			5170
taaatgcggt tttaccaagt tttcccttga aaatgtaatt cctttatgga gatttattgt			5230
gcagccctaa gcttccttcc catttcatga atataaggct tctagaattg gactggcagg			5290
ggaaagaatg gtagagacag aaattaagac tttatccttg tttgcttgta aactattatt			5350
ttcttgctaa tgtaacattt gtctgttcca gtgatgtaag gatattaagt tattaagcta			5410
aatattaatt ttcaaaaaata gtccttcttt aacttagata tttcatagct ggatttagga			5470
agatctgtta ttctggaagt actaaaaaga ataatacaac gtacaatgtc tgcattcact			5530
aattcatgtt ccagaagagg aaataatgaa gatatactca gtagagtact aggtgggagg			5590
atatggaaat ttgctcataa aatctcttat aaaacgtgca tataacaaaa tgacaccag			5650
taggcctgca ttacatttac atgaccgtgt ttatttgcca tcaataaaac tgagtactga			5710
caccagacaa agactccaaa gtcataaaat agcctatgac caactgcagc aagacaggag			5770
gtcagctcgc ctataatggt gcttaagtg tgaattgatg aattttctgt actcaccatt			5830
tgaagttagt taaggagaac tttatttttt taaaaaaagt aaatggcaac cactagtgtg			5890
ctcatcctga actgttact caaatccact cgttttttaa agcaaaaatta tcttgtgatt			5950
ttaagaaaag agttttctat ttattttaaga aagtaacaat gcagtctgca agctttcagt			6010
agttttctag tgctatatcc atcctgtaaa actcttacta cgtaaccagt aatcacaagg			6070


```

aaagtgtccc ctttgcatat ttcttttaaaa ttcttttcttt ggaaagtatg atgttgataa 6130
ttaacttacc cttatctgcc aaaaccagag caaaatgcta aatacgttat tgctaatacag 6190
tggtctcaaa tcgatttgcc tccctttgcc tcgtctgagg gctgtaagcc tgaagatag 6250
ggcaagcacc aagtcagttt ccaaaattgc ccctcagctg ctttaagtga ctcagcaccc 6310
tgccctcagct tcagcaggcg taggctcacc ctgggcggag caaagtatgg gccagggaga 6370
actacagcta cgaagacctg ctgtogagtt gagaaaaggg gagaatttat ggtctgaatt 6430
ttctaactgt cctctttctt gggctctaaag ctcataatac acaaaggctt ccagacctga 6490
gccacaccca ggccctatcc tgaacaggag actaaacaga ggcaaataca ccctaggaaa 6550
tacttgcatt ctgccctacg gttagtacca ggactgaggt catttctact ggaaaagatt 6610
gtgagattga acttatctga tcgcttgaga ctctaatag gcaggagtca aggccactag 6670
aaaattgaca gttaagagcc aaaagttttt aaaatatgct actctgaaaa atctcgtgaa 6730
ggctgtagga aaaggagaa tcttccatgt tgggtgtttt cctgtaaaga tcagtttggg 6790
gtatgatata agcagggtatt aataaaaata acacaccaa gagttacgta aaacatgttt 6850
tattaatttt ggtccccacg tacagacatt ttatttctat tttgaaatga gttatctatt 6910
ttcataaaaag taaaacacta ttaagtgtct gttttatgtg aaataacttg aatgttggtc 6970
ctataaaaaa tagatcataa ctcatgatat gtttgtaatc atggtaattt agatttttat 7030
gaggaatgag tatctggaaa tattgtagca atacttggtt taaaattttg gacctgagac 7090
actgtggctg tctaattgaa tcttttaaaa attctctgca ttgtcagtaa atgtagtata 7150
ttattgtaca gctactcata attttttaaa gtttatgaag ttatatattt caaataaaaa 7210
ctttcctata t

```

<210> 20

<211> 1177

<212> PRT

<213> Homo sapiens

<400> 20

```

Met Trp Arg Trp Ile Arg Gln Gln Leu Gly Phe Asp Pro Pro His Gln
1 5 10 15
Ser Asp Thr Arg Thr Ile Tyr Val Ala His Arg Phe Pro Gln Asn Gly
20 25 30
Leu Tyr Thr Pro Gln Lys Phe Ile Asp Asn Arg Ile Ile Ser Ser Lys
35 40 45
Tyr Thr Val Trp Asn Phe Val Pro Lys Asn Leu Phe Glu Gln Phe Arg
50 55 60
Arg Val Ala Asn Phe Tyr Phe Leu Ile Ile Phe Leu Val Gln Leu Met
65 70 75 80
Ile Asp Thr Pro Thr Ser Pro Val Thr Ser Gly Leu Pro Leu Phe Phe
85 90 95
Val Ile Thr Val Thr Ala Ile Lys Gln Gly Tyr Glu Asp Trp Leu Arg
100 105 110
His Asn Ser Asp Asn Glu Val Asn Gly Ala Pro Val Tyr Val Val Arg
115 120 125
Ser Gly Gly Leu Val Lys Thr Arg Ser Lys Asn Ile Arg Val Gly Asp
130 135 140
Ile Val Arg Ile Ala Lys Asp Glu Ile Phe Pro Ala Asp Leu Val Leu
145 150 155 160
Leu Ser Ser Asp Arg Leu Asp Gly Ser Cys His Val Thr Thr Ala Ser
165 170 175
Leu Asp Gly Glu Thr Asn Leu Lys Thr His Val Ala Val Pro Glu Thr
180 185 190
Ala Leu Leu Gln Thr Val Ala Asn Leu Asp Thr Leu Val Ala Val Ile
195 200 205
Glu Cys Gln Gln Pro Glu Ala Asp Leu Tyr Arg Phe Met Gly Arg Met
210 215 220
Ile Ile Thr Gln Gln Met Glu Glu Ile Val Arg Pro Leu Gly Pro Glu
225 230 235 240
Ser Leu Leu Leu Arg Gly Ala Arg Leu Lys Asn Thr Lys Glu Ile Phe
245 250 255
Gly Val Ala Val Tyr Thr Gly Met Glu Thr Lys Met Ala Leu Asn Tyr

```

1004531001

			260								265								270				
Lys	Ser	Lys	Ser	Gln	Lys	Arg	Ser	Ala	Val	Glu	Lys	Ser	Met	Asn	Thr								
		275					280					285											
Phe	Leu	Ile	Ile	Tyr	Leu	Val	Ile	Leu	Ile	Ser	Glu	Ala	Val	Ile	Ser								
		290				295					300												
Thr	Ile	Leu	Lys	Tyr	Thr	Trp	Gln	Ala	Glu	Glu	Lys	Trp	Asp	Glu	Pro								
305					310					315					320								
Trp	Tyr	Asn	Gln	Lys	Thr	Glu	His	Gln	Arg	Asn	Ser	Ser	Lys	Ile	Leu								
				325					330					335									
Arg	Phe	Ile	Ser	Asp	Phe	Leu	Ala	Phe	Leu	Val	Leu	Tyr	Asn	Phe	Ile								
				340				345					350										
Ile	Pro	Ile	Ser	Leu	Tyr	Val	Thr	Val	Glu	Met	Gln	Lys	Phe	Leu	Gly								
		355					360					365											
Ser	Phe	Phe	Ile	Gly	Trp	Asp	Leu	Asp	Leu	Tyr	His	Glu	Glu	Ser	Asp								
		370				375					380												
Gln	Lys	Ala	Gln	Val	Asn	Thr	Ser	Asp	Leu	Asn	Glu	Glu	Leu	Gly	Gln								
385					390					395					400								
Val	Glu	Tyr	Val	Phe	Thr	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Glu	Asn	Glu								
				405					410					415									
Met	Gln	Phe	Arg	Glu	Cys	Ser	Ile	Asn	Gly	Met	Lys	Tyr	Gln	Glu	Ile								
			420					425					430										
Asn	Gly	Arg	Leu	Val	Pro	Glu	Gly	Pro	Thr	Pro	Asp	Ser	Ser	Glu	Gly								
		435					440					445											
Asn	Leu	Ser	Tyr	Leu	Ser	Ser	Leu	Ser	His	Leu	Asn	Asn	Leu	Ser	His								
		450				455					460												
Leu	Thr	Thr	Ser	Ser	Ser	Phe	Arg	Thr	Ser	Pro	Glu	Asn	Glu	Thr	Glu								
465					470					475					480								
Leu	Ile	Lys	Glu	His	Asp	Leu	Phe	Phe	Lys	Ala	Val	Ser	Leu	Cys	His								
				485					490					495									
Thr	Val	Gln	Ile	Ser	Asn	Val	Gln	Thr	Asp	Cys	Thr	Gly	Asp	Gly	Pro								
			500					505					510										
Trp	Gln	Ser	Asn	Leu	Ala	Pro	Ser	Gln	Leu	Glu	Tyr	Tyr	Ala	Ser	Ser								
		515					520					525											
Pro	Asp	Glu	Lys	Ala	Leu	Val	Glu	Ala	Ala	Ala	Arg	Ile	Gly	Ile	Val								
		530				535					540												
Phe	Ile	Gly	Asn	Ser	Glu	Thr	Met	Glu	Val	Lys	Thr	Leu	Gly	Lys									
545					550				555					560									

<220>

<221> CDS

<222> (1)...(3534)

<400> 21

atg tgg cgc tgg atc cgg cag cag ctg ggt ttt gac cca cca cat cag	48
Met Trp Arg Trp Ile Arg Gln Gln Leu Gly Phe Asp Pro Pro His Gln	
1 5 10 15	
agt gac aca aga acc atc tac gta gcc cac agg ttt cct cag aat ggc	96
Ser Asp Thr Arg Thr Ile Tyr Val Ala His Arg Phe Pro Gln Asn Gly	
20 25 30	
ctt tac aca cct cag aaa ttt ata gat aac agg atc att tca tct aag	144
Leu Tyr Thr Pro Gln Lys Phe Ile Asp Asn Arg Ile Ile Ser Ser Lys	
35 40 45	
tac act gtg tgg aat ttt gtt cca aaa aat tta ttt gaa cag ttc aga	192
Tyr Thr Val Trp Asn Phe Val Pro Lys Asn Leu Phe Glu Gln Phe Arg	
50 55 60	
aga gtg gca aac ttt tat ttt ctt att ata ttt ttg gtt cag ctt atg	240
Arg Val Ala Asn Phe Tyr Phe Leu Ile Ile Phe Leu Val Gln Leu Met	
65 70 75 80	
att gat aca cct acc agt cca gtt acc agt gga ctt cca tta ttc ttt	288
Ile Asp Thr Pro Thr Ser Pro Val Thr Ser Gly Leu Pro Leu Phe Phe	
85 90 95	
gtg ata aca gta act gcc ata aag cag gga tat gaa gat tgg tta cgg	336
Val Ile Thr Val Thr Ala Ile Lys Gln Gly Tyr Glu Asp Trp Leu Arg	
100 105 110	
cat aac tca gat aat gaa gta aat gga gct cct gtt tat gtt gtt cga	384
His Asn Ser Asp Asn Glu Val Asn Gly Ala Pro Val Tyr Val Val Arg	
115 120 125	
agt ggt ggc ctt gta aaa act aga tca aaa aac att cgg gtg ggt gat	432
Ser Gly Gly Leu Val Lys Thr Arg Ser Lys Asn Ile Arg Val Gly Asp	
130 135 140	
att gtt cga ata gcc aaa gat gaa att ttt cct gca gac ttg gtg ctt	480
Ile Val Arg Ile Ala Lys Asp Glu Ile Phe Pro Ala Asp Leu Val Leu	
145 150 155 160	
ctg tcc tca gat cga ctg gat ggt tcc tgt cac gtt aca act gct agt	528
Leu Ser Ser Asp Arg Leu Asp Gly Ser Cys His Val Thr Thr Ala Ser	
165 170 175	
ttg gac gga gaa act aac ctg aag aca cat gtg gca gtt cca gaa aca	576
Leu Asp Gly Glu Thr Asn Leu Lys Thr His Val Ala Val Pro Glu Thr	
180 185 190	
gca tta tta caa aca gtt gcc aat ttg gac act cta gta gct gta ata	624
Ala Leu Leu Gln Thr Val Ala Asn Leu Asp Thr Leu Val Ala Val Ile	
195 200 205	
gaa tgc cag caa cca gaa gca gac tta tac aga ttc atg gga cga atg	672
Glu Cys Gln Gln Pro Glu Ala Asp Leu Tyr Arg Phe Met Gly Arg Met	
210 215 220	

T044269400T

Leu	Thr	Thr	Ser	Ser	Ser	Phe	Arg	Thr	Ser	Pro	Glu	Asn	Glu	Thr	Glu	
465					470					475					480	
cta	att	aaa	gaa	cat	gat	ctc	ttc	ttt	aaa	gca	gtc	agt	ctc	tgt	cac	1488
Leu	Ile	Lys	Glu	His	Asp	Leu	Phe	Phe	Lys	Ala	Val	Ser	Leu	Cys	His	
				485					490					495		
act	gta	cag	att	agc	aat	gtt	caa	act	gac	tgc	act	ggt	gat	ggt	ccc	1536
Thr	Val	Gln	Ile	Ser	Asn	Val	Gln	Thr	Asp	Cys	Thr	Gly	Asp	Gly	Pro	
			500					505					510			
tgg	caa	tcc	aac	ctg	gca	cca	tcg	cag	ttg	gag	tac	tat	gca	tct	tca	1584
Trp	Gln	Ser	Asn	Leu	Ala	Pro	Ser	Gln	Leu	Glu	Tyr	Tyr	Ala	Ser	Ser	
		515					520					525				
cca	gat	gaa	aag	gct	cta	gta	gaa	gct	gct	gca	agg	att	ggt	att	gtg	1632
Pro	Asp	Glu	Lys	Ala	Leu	Val	Glu	Ala	Ala	Ala	Arg	Ile	Gly	Ile	Val	
	530					535					540					
ttt	att	ggc	aat	tct	gaa	gaa	act	atg	gag	gtt	aaa	act	ctt	gga	aaa	1680
Phe	Ile	Gly	Asn	Ser	Glu	Glu	Thr	Met	Glu	Val	Lys	Thr	Leu	Gly	Lys	
545					550					555					560	
ctg	gaa	cgg	tac	aaa	ctg	ctt	cat	att	ctg	gaa	ttt	gat	tca	gat	cgt	1728
Leu	Glu	Arg	Tyr	Lys	Leu	Leu	His	Ile	Leu	Glu	Phe	Asp	Ser	Asp	Arg	
				565					570					575		
agg	aga	atg	agt	gta	att	gtt	cag	gca	cct	tca	ggt	gag	aag	tta	tta	1776
Arg	Arg	Met	Ser	Val	Ile	Val	Gln	Ala	Pro	Ser	Gly	Glu	Lys	Leu	Leu	
			580					585					590			
ttt	gct	aaa	gga	gct	gag	tca	tca	att	ctc	cct	aaa	tgt	ata	ggt	gga	1824
Phe	Ala	Lys	Gly	Ala	Glu	Ser	Ser	Ile	Leu	Pro	Lys	Cys	Ile	Gly	Gly	
		595					600					605				
gaa	ata	gaa	aaa	acc	aga	att	cat	gta	gat	gaa	ttt	gct	ttg	aaa	ggg	1872
Glu	Ile	Glu	Lys	Thr	Arg	Ile	His	Val	Asp	Glu	Phe	Ala	Leu	Lys	Gly	
	610					615					620					
cta	aga	act	ctg	tgt	ata	gca	tat	aga	aaa	ttt	aca	tca	aaa	gag	tat	1920
Leu	Arg	Thr	Leu	Cys	Ile	Ala	Tyr	Arg	Lys	Phe	Thr	Ser	Lys	Glu	Tyr	
625					630					635					640	
gag	gaa	ata	gat	aaa	cgc	ata	ttt	gaa	gcc	agg	act	gcc	ttg	cag	cag	1968
Glu	Glu	Ile	Asp	Lys	Arg	Ile	Phe	Glu	Ala	Arg	Thr	Ala	Leu	Gln	Gln	
				645				650						655		
cgg	gaa	gag	aaa	ttg	gca	gct	gtt	ttc	cag	ttc	ata	gag	aaa	gac	ctg	2016
Arg	Glu	Glu	Lys	Leu	Ala	Ala	Val	Phe	Gln	Phe	Ile	Glu	Lys	Asp	Leu	
			660					665						670		
ata	tta	ctt	gga	gcc	aca	gca	gta	gaa	gac	aga	cta	caa	gat	aaa	gtt	2064
Ile	Leu	Leu	Gly	Ala	Thr	Ala	Val	Glu	Asp	Arg	Leu	Gln	Asp	Lys	Val	
		675					680					685				
cga	gaa	act	att	gaa	gca	ttg	aga	atg	gct	ggt	atc	aaa	gta	tgg	gta	2112
Arg	Glu	Thr	Ile	Glu	Ala	Leu	Arg	Met	Ala	Gly	Ile	Lys	Val	Trp	Val	
	690					695				700						
ctt	act	ggg	gat	aaa	cat	gaa	aca	gct	gtt	agt	gtg	agt	tta	tca	tgt	2160
Leu	Thr	Gly	Asp	Lys	His	Glu	Thr	Ala	Val	Ser	Val	Ser	Leu	Ser	Cys	

T00434000

705	710	715	720	
ggc cat ttt cat aga acc atg aac atc ctt gaa ctt ata aac cag aaa				2208
Gly His Phe His Arg Thr Met Asn Ile Leu Glu Leu Ile Asn Gln Lys	725	730	735	
tca gac agc gag tgt gct gaa caa ttg agg cag ctt gcc aga aga att				2256
Ser Asp Ser Glu Cys Ala Glu Gln Leu Arg Gln Leu Ala Arg Arg Ile	740	745	750	
aca gag gat cat gtg att cag cat ggg ctg gta gtg gat ggg acc agc				2304
Thr Glu Asp His Val Ile Gln His Gly Leu Val Val Asp Gly Thr Ser	755	760	765	
cta tct ctt gca ctc agg gag cat gaa aaa cta ttt atg gaa gtt tgc				2352
Leu Ser Leu Ala Leu Arg Glu His Glu Lys Leu Phe Met Glu Val Cys	770	775	780	
aga aat tgt tca gct gta tta tgc tgt cgt atg gct cca ctg cag aaa				2400
Arg Asn Cys Ser Ala Val Leu Cys Cys Arg Met Ala Pro Leu Gln Lys	785	790	800	
gca aaa gta ata aga cta ata aaa ata tca cct gag aaa cct ata aca				2448
Ala Lys Val Ile Arg Leu Ile Lys Ile Ser Pro Glu Lys Pro Ile Thr	805	810	815	
ttg gct gtt ggt gat ggt gct aat gac gta agc atg ata caa gaa gcc				2496
Leu Ala Val Gly Asp Gly Ala Asn Asp Val Ser Met Ile Gln Glu Ala	820	825	830	
cat gtt ggc ata gga atc atg ggt aaa gaa gga aga cag gct gca aga				2544
His Val Gly Ile Gly Ile Met Gly Lys Glu Gly Arg Gln Ala Ala Arg	835	840	845	
aac agt gac tat gca ata gcc aga ttt aag ttc ctc tcc aaa ttg ctt				2592
Asn Ser Asp Tyr Ala Ile Ala Arg Phe Lys Phe Leu Ser Lys Leu Leu	850	855	860	
ttt gtt cat ggt cat ttt tat tat att aga ata gct acc ctt gta cag				2640
Phe Val His Gly His Phe Tyr Tyr Ile Arg Ile Ala Thr Leu Val Gln	865	870	875	880
tat ttt ttt tat aag aat gtg tgc ttt atc aca ccc cag ttt tta tat				2688
Tyr Phe Phe Tyr Lys Asn Val Cys Phe Ile Thr Pro Gln Phe Leu Tyr	885	890	895	
cag ttc tac tgt ttg ttt tct cag caa aca ttg tat gac agc gtg tac				2736
Gln Phe Tyr Cys Leu Phe Ser Gln Gln Thr Leu Tyr Asp Ser Val Tyr	900	905	910	
ctg act tta tac aat att tgt ttt act tcc cta cct att ctg ata tat				2784
Leu Thr Leu Tyr Asn Ile Cys Phe Thr Ser Leu Pro Ile Leu Ile Tyr	915	920	925	
agt ctt ttg gaa cag cat gta gac cct cat gtg tta caa aat aag ccc				2832
Ser Leu Leu Glu Gln His Val Asp Pro His Val Leu Gln Asn Lys Pro	930	935	940	
acc ctt tat cga gac att agt aaa aac cgc ctc tta agt att aaa aca				2880
Thr Leu Tyr Arg Asp Ile Ser Lys Asn Arg Leu Leu Ser Ile Lys Thr	945	950	955	960

Total bases

ttt ctt tat tgg acc atc ctg ggc ttc agt cat gcc ttt att ttc ttt 2928
 Phe Leu Tyr Trp Thr Ile Leu Gly Phe Ser His Ala Phe Ile Phe Phe
 965 970 975

ttt gga tcc tat tta cta ata ggg aaa gat aca tct ctg ctt gga aat 2976
 Phe Gly Ser Tyr Leu Leu Ile Gly Lys Asp Thr Ser Leu Leu Gly Asn
 980 985 990

ggc cag atg ttt gga aac tgg aca ttt ggc act ttg gtc ttc aca gtc 3024
 Gly Gln Met Phe Gly Asn Trp Thr Phe Gly Thr Leu Val Phe Thr Val
 995 1000 1005

atg gtt att aca gtc aca gta aag atg gct ctg gaa act cat ttt tgg 3072
 Met Val Ile Thr Val Thr Val Lys Met Ala Leu Glu Thr His Phe Trp
 1010 1015 1020

act tgg atc aac cat ctc gtt acc tgg gga tct att ata ttt tat ttt 3120
 Thr Trp Ile Asn His Leu Val Thr Trp Gly Ser Ile Ile Phe Tyr Phe
 1025 1030 1035 1040

gta ttt tcc ttg ttt tat gga ggg att ctc tgg cca ttt ttg ggc tcc 3168
 Val Phe Ser Leu Phe Tyr Gly Gly Ile Leu Trp Pro Phe Leu Gly Ser
 1045 1050 1055

cag aat atg tat ttt gtg ttt att cag ctc ctg tca agt ggt tct gct 3216
 Gln Asn Met Tyr Phe Val Phe Ile Gln Leu Leu Ser Ser Gly Ser Ala
 1060 1065 1070

tgg ttt gcc ata atc ctc atg gtt gtt aca tgt cta ttt ctt gat atc 3264
 Trp Phe Ala Ile Ile Leu Met Val Val Thr Cys Leu Phe Leu Asp Ile
 1075 1080 1085

ata aag aag gtc ttt gac cga cac ctc cac cct aca agt act gaa aag 3312
 Ile Lys Lys Val Phe Asp Arg His Leu His Pro Thr Ser Thr Glu Lys
 1090 1095 1100

gca cag ctt act gaa aca aat gca ggt atc aag tgc ttg gac tcc atg 3360
 Ala Gln Leu Thr Glu Thr Asn Ala Gly Ile Lys Cys Leu Asp Ser Met
 1105 1110 1115 1120

tgc tgt ttc ccg gaa gga gaa gca gcg tgt gca tct gtt gga aga atg 3408
 Cys Cys Phe Pro Glu Gly Glu Ala Ala Cys Ala Ser Val Gly Arg Met
 1125 1130 1135

ctg gaa cga gtt ata gga aga tgt agt cca acc cac atc agc agt tca 3456
 Leu Glu Arg Val Ile Gly Arg Cys Ser Pro Thr His Ile Ser Ser Ser
 1140 1145 1150

tgg agt gca tgc gat cct ttc tat acc aac gac agg agc atc ttg act 3504
 Trp Ser Ala Ser Asp Pro Phe Tyr Thr Asn Asp Arg Ser Ile Leu Thr
 1155 1160 1165

ctc tcc aca atg gac tca tct act tgt taa 3534
 Leu Ser Thr Met Asp Ser Ser Thr Cys *
 1170 1175

<210> 22
 <211> 4198
 <212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (156) \dots (3410)$

<400> 22

```

ggagtcgacc  cacgcgtccg  cattgagaca  atgcctccac  aaatacttga  tgcaaaattc  60
agtaagacag  cacttgittg  atcaccatta  tagtttctga  caaattgttc  tcaaaaaggt  120
accagctgga  ggatgagttc  gcgcatttgg  atgaa  atg  cca  cta  atg  atg  tct      173
                               Met  Pro  Leu  Met  Met  Ser
                               1      5

```

gaa gaa ggc ttt gag aat gag gaa agt gat tac cac acc tta cca cga 221
Glu Glu Gly Phe Glu Asn Glu Glu Ser Asp Tyr His Thr Leu Pro Arg
10 15 20

gcc agg ata atg caa agg aaa aga gga ctg gag tgg ttt gtc tgt gat 269
Ala Arg Ile Met Gln Arg Lys Arg Gly Leu Glu Trp Phe Val Cys Asp
25 30 35

ggc tgg aag ttc ctc tgt acc agt tgc tgt ggt tgg ctg ata aat att 317
Gly Trp Lys Phe Leu Cys Thr Ser Cys Cys Gly Trp Leu Ile Asn Ile
40 45 50

tgt cga aga aag aaa gag ctg aaa gct cgc aca gta tgg ctt gga tgt 365
Cys Arg Arg Lys Lys Glu Leu Lys Ala Arg Thr Val Trp Leu Gly Cys
55 60 65 70

cct gaa aag tgt gaa gaa aaa cat ccc agg aat tct ata aaa aat caa 413
Pro Glu Lys Cys Glu Glu Lys His Pro Arg Asn Ser Ile Lys Asn Gln
75 80 85

```

aaa tac aat gtg ttt acc ttt ata cct ggg gtt ttg tat gaa caa ttc    461
Lys Tyr Asn Val Phe Thr Phe Ile Pro Gly Val Leu Tyr Glu Gln Phe
          90                      95                      100

```

aag ttt ttc ttg aat ctc tat ttt cta gtg ata tcc tgc tca cag ttt 509
Lys Phe Phe Leu Asn Leu Tyr Phe Leu Val Ile Ser Cys Ser Gln Phe
105 110 115

gta cca gca ttg aaa ata ggc tat ctc tac acc tac tgg gct cct ctg 557
Val Pro Ala Leu Lys Ile Gly Tyr Leu Tyr Thr Tyr Trp Ala Pro Leu
120 125 130

gga ttt gtc ttg gct gtt act atg aca cgg gaa gca att gat gaa ttt 605
Gly Phe Val Leu Ala Val Thr Met Thr Arg Glu Ala Ile Asp Glu Phe
135 140 145 150

cgg cgt ttt cag cgt gac aag gaa gtg aat tca caa cta tat agc aag 653
Arg Arg Phe Gln Arg Asp Lys Glu Val Asn Ser Gln Leu Tyr Ser Lys
155 160 165

ctt aca gta aga ggt aaa gtg caa gtt aag agt tca gac ata caa gtt 701
 Leu Thr Val Arg Gly Lys Val Gln Val Lys Ser Ser Asp Ile Gln Val
 170 175 180

gga gac ctc atc ata gtg gaa aag aat caa aga att cca tgc gac atg 749
Gly Asp Leu Ile Ile Val Glu Lys Asn Gln Arg Ile Pro Ser Asp Met
185 190 195

gtg ttt ctt agg act tca gaa aaa gca ggt tcg tgt ttt att cga act	797
Val Phe Leu Arg Thr Ser Glu Lys Ala Gly Ser Cys Phe Ile Arg Thr	
200 205 210	
gat caa cta gat ggt gaa act gac tgg aag ctg aag gtg gca gtg agc	845
Asp Gln Leu Asp Gly Glu Thr Asp Trp Lys Leu Lys Val Ala Val Ser	
215 220 225 230	
tgc acg caa cag ctg ccg gct ctg ggg gac ctt ttt tct atc agt gct	893
Cys Thr Gln Gln Leu Pro Ala Leu Gly Asp Leu Phe Ser Ile Ser Ala	
235 240 245	
tat gtt tat gct cag aaa cca caa atg gac att cac agt ttc gaa ggc	941
Tyr Val Tyr Ala Gln Lys Pro Gln Met Asp Ile His Ser Phe Glu Gly	
250 255 260	
aca ttt acc agg gaa gac agt gac ccg ccc att cat gaa agt ctc agc	989
Thr Phe Thr Arg Glu Asp Ser Asp Pro Pro Ile His Glu Ser Leu Ser	
265 270 275	
ata gaa aat aca ttg tgg gca agc acc att gtt gca tca ggt act gta	1037
Ile Glu Asn Thr Leu Trp Ala Ser Thr Ile Val Ala Ser Gly Thr Val	
280 285 290	
ata ggt gtt gtc att tat acc gga aaa gag act cga agt gta atg aac	1085
Ile Gly Val Val Ile Tyr Thr Gly Lys Glu Thr Arg Ser Val Met Asn	
295 300 305 310	
aca tcc aat cca aaa aat aag gtt ggt ttg ttg gac ctt gaa ctc aat	1133
Thr Ser Asn Pro Lys Asn Lys Val Gly Leu Leu Asp Leu Glu Leu Asn	
315 320 325	
cgg ctg acg aaa gcg cta ttt ttg gct tta gtt gct ctt tcc att gtt	1181
Arg Leu Thr Lys Ala Leu Phe Leu Ala Leu Val Ala Leu Ser Ile Val	
330 335 340	
atg gta acc tta caa gga ttt gtg ggt cca tgg tac cgc aat ctt ttt	1229
Met Val Thr Leu Gln Gly Phe Val Gly Pro Trp Tyr Arg Asn Leu Phe	
345 350 355	
cgg ttc ctt ctc ctc ttt tct tac atc att ccc ata agt ttg cgt gtg	1277
Arg Phe Leu Leu Leu Phe Ser Tyr Ile Ile Pro Ile Ser Leu Arg Val	
360 365 370	
aac ttg gac atg ggc aaa gcg gtg tat gga tgg atg atg atg aaa gat	1325
Asn Leu Asp Met Gly Lys Ala Val Tyr Gly Trp Met Met Met Lys Asp	
375 380 385 390	
gag aac atc cct ggc acg gtc gtt cgg acc agc act atc cca gag gaa	1373
Glu Asn Ile Pro Gly Thr Val Val Arg Thr Ser Thr Ile Pro Glu Glu	
395 400 405	
ctt ggg cgc ctg gtg tat tta ttg aca gac aaa aca gga acc ctc acc	1421
Leu Gly Arg Leu Val Tyr Leu Leu Thr Asp Lys Thr Gly Thr Leu Thr	
410 415 420	
cag aat gaa atg ata ttt aag cgg ctg cac ctg ggc acc gtg tcc tat	1469
Gln Asn Glu Met Ile Phe Lys Arg Leu His Leu Gly Thr Val Ser Tyr	
425 430 435	
ggc gcc gac acg atg gat gag atc cag agc cat gtc agg gac tcc tac	1517

1004631401

680	685	690	
gac gtg cgg ccc acg ctg gag atg ctg cgc aac gcc ggg atc aag ata			2285
Asp Val Arg Pro Thr Leu Glu Met Leu Arg Asn Ala Gly Ile Lys Ile			
695	700	705	710
tggt atg cta aca ggc gat aaa ctc gag aca gct acc tgc att gcc aaa			2333
Trp Met Leu Thr Gly Asp Lys Leu Glu Thr Ala Thr Cys Ile Ala Lys			
	715	720	725
agt tca cat ctc gtg tct aga aca caa gat att cat att ttc aga cag			2381
Ser Ser His Leu Val Ser Arg Thr Gln Asp Ile His Ile Phe Arg Gln			
	730	735	740
gta acc agt cgg gga gag gca cat ttg gag ctg aat gca ttt cga agg			2429
Val Thr Ser Arg Gly Glu Ala His Leu Glu Leu Asn Ala Phe Arg Arg			
	745	750	755
aag cat gat tgt gca cta gtc ata tct ggg gac tct ctg gag gtt tgt			2477
Lys His Asp Cys Ala Leu Val Ile Ser Gly Asp Ser Leu Glu Val Cys			
	760	765	770
cta aag tac tac gag cat gaa ttt gtg gag ctg gcc tgc cag tgc cct			2525
Leu Lys Tyr Tyr Glu His Glu Phe Val Glu Leu Ala Cys Gln Cys Pro			
	775	780	785
gcc gtg gtt tgc tgc cgc tgc tca ccc acc cag aag gcc cgc att gtg			2573
Ala Val Val Cys Cys Arg Cys Ser Pro Thr Gln Lys Ala Arg Ile Val			
	795	800	805
aca ctg ctg cag cag cac aca ggg aga cgc acc tgc gcc atc ggt gat			2621
Thr Leu Leu Gln Gln His Thr Gly Arg Arg Thr Cys Ala Ile Gly Asp			
	810	815	820
gga gga aat gat gtc agc atg att cag gca gca gac tgt ggg att ggg			2669
Gly Gly Asn Asp Val Ser Met Ile Gln Ala Ala Asp Cys Gly Ile Gly			
	825	830	835
att gag gga aag gag ggt aaa cag gcc tcg ctg gcg gcc gac ttc tcc			2717
Ile Glu Gly Lys Glu Gly Lys Gln Ala Ser Leu Ala Ala Asp Phe Ser			
	840	845	850
atc acg cag ttc cgg cac ata ggc agg ctg ctc atg gtg cac ggg cgg			2765
Ile Thr Gln Phe Arg His Ile Gly Arg Leu Leu Met Val His Gly Arg			
	855	860	865
aac agc tac aag agg tcg gcg gca ctc ggc cag ttc gtc atg cac agg			2813
Asn Ser Tyr Lys Arg Ser Ala Ala Leu Gly Gln Phe Val Met His Arg			
	875	880	885
ggc ctt atc atc tcc acc atg cag gct gtg ttt tcc tca gtc ttc tac			2861
Gly Leu Ile Ile Ser Thr Met Gln Ala Val Phe Ser Ser Val Phe Tyr			
	890	895	900
ttc gca tcc gtc cct ttg tat cag ggc ttc ctc atg gtg ggg tat gcc			2909
Phe Ala Ser Val Pro Leu Tyr Gln Gly Phe Leu Met Val Gly Tyr Ala			
	905	910	915
acc ata tac acc atg ttc cca gtg ttc tcc tta gtg ctg gac cag gac			2957
Thr Ile Tyr Thr Met Phe Pro Val Phe Ser Leu Val Leu Asp Gln Asp			
	920	925	930

10042001

Met Pro Leu Met Met Ser Glu Glu Gly Phe Glu Asn Glu Glu Ser Asp
 1 5 10 15
 Tyr His Thr Leu Pro Arg Ala Arg Ile Met Gln Arg Lys Arg Gly Leu
 20 25 30
 Glu Trp Phe Val Cys Asp Gly Trp Lys Phe Leu Cys Thr Ser Cys Cys
 35 40 45
 Gly Trp Leu Ile Asn Ile Cys Arg Arg Lys Lys Glu Leu Lys Ala Arg
 50 55 60
 Thr Val Trp Leu Gly Cys Pro Glu Lys Cys Glu Glu Lys His Pro Arg
 65 70 75 80
 Asn Ser Ile Lys Asn Gln Lys Tyr Asn Val Phe Thr Phe Ile Pro Gly
 85 90 95
 Val Leu Tyr Glu Gln Phe Lys Phe Phe Leu Asn Leu Tyr Phe Leu Val
 100 105 110
 Ile Ser Cys Ser Gln Phe Val Pro Ala Leu Lys Ile Gly Tyr Leu Tyr
 115 120 125
 Thr Tyr Trp Ala Pro Leu Gly Phe Val Leu Ala Val Thr Met Thr Arg
 130 135 140
 Glu Ala Ile Asp Glu Phe Arg Arg Phe Gln Arg Asp Lys Glu Val Asn
 145 150 155 160
 Ser Gln Leu Tyr Ser Lys Leu Thr Val Arg Gly Lys Val Gln Val Lys
 165 170 175
 Ser Ser Asp Ile Gln Val Gly Asp Leu Ile Ile Val Glu Lys Asn Gln
 180 185 190
 Arg Ile Pro Ser Asp Met Val Phe Leu Arg Thr Ser Glu Lys Ala Gly
 195 200 205
 Ser Cys Phe Ile Arg Thr Asp Gln Leu Asp Gly Glu Thr Asp Trp Lys
 210 215 220
 Leu Lys Val Ala Val Ser Cys Thr Gln Gln Leu Pro Ala Leu Gly Asp
 225 230 235 240
 Leu Phe Ser Ile Ser Ala Tyr Val Tyr Ala Gln Lys Pro Gln Met Asp
 245 250 255
 Ile His Ser Phe Glu Gly Thr Phe Thr Arg Glu Asp Ser Asp Pro Pro
 260 265 270
 Ile His Glu Ser Leu Ser Ile Glu Asn Thr Leu Trp Ala Ser Thr Ile
 275 280 285
 Val Ala Ser Gly Thr Val Ile Gly Val Val Ile Tyr Thr Gly Lys Glu
 290 295 300
 Thr Arg Ser Val Met Asn Thr Ser Asn Pro Lys Asn Lys Val Gly Leu
 305 310 315 320
 Leu Asp Leu Glu Leu Asn Arg Leu Thr Lys Ala Leu Phe Leu Ala Leu
 325 330 335
 Val Ala Leu Ser Ile Val Met Val Thr Leu Gln Gly Phe Val Gly Pro
 340 345 350
 Trp Tyr Arg Asn Leu Phe Arg Phe Leu Leu Leu Phe Ser Tyr Ile Ile
 355 360 365
 Pro Ile Ser Leu Arg Val Asn Leu Asp Met Gly Lys Ala Val Tyr Gly
 370 375 380
 Trp Met Met Met Lys Asp Glu Asn Ile Pro Gly Thr Val Val Arg Thr
 385 390 395 400
 Ser Thr Ile Pro Glu Glu Leu Gly Arg Leu Val Tyr Leu Leu Thr Asp
 405 410 415
 Lys Thr Gly Thr Leu Thr Gln Asn Glu Met Ile Phe Lys Arg Leu His
 420 425 430
 Leu Gly Thr Val Ser Tyr Gly Ala Asp Thr Met Asp Glu Ile Gln Ser
 435 440 445
 His Val Arg Asp Ser Tyr Ser Gln Met Gln Ser Gln Ala Gly Gly Asn
 450 455 460
 Asn Thr Gly Ser Thr Pro Leu Arg Lys Ala Gln Ser Ser Ala Pro Lys
 465 470 475 480
 Val Arg Lys Ser Val Ser Ser Arg Ile His Glu Ala Val Lys Ala Ile

100463
 6254007

				485					490					495			
Val	Leu	Cys	His	Asn	Val	Thr	Pro	Val	Tyr	Glu	Ser	Arg	Ala	Gly	Val		
			500						505					510			
Thr	Glu	Glu	Thr	Glu	Phe	Ala	Glu	Ala	Asp	Gln	Asp	Phe	Ser	Asp	Glu		
		515						520					525				
Asn	Arg	Thr	Tyr	Gln	Ala	Ser	Ser	Pro	Asp	Glu	Val	Ala	Leu	Val	Gln		
		530					535					540					
Trp	Thr	Glu	Ser	Val	Gly	Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Thr	Ser		
545					550					555					560		
Met	Gln	Leu	Lys	Thr	Pro	Ser	Gly	Gln	Val	Leu	Ser	Phe	Cys	Ile	Leu		
				565					570					575			
Gln	Leu	Phe	Pro	Phe	Thr	Ser	Glu	Ser	Lys	Arg	Met	Gly	Val	Ile	Val		
			580						585					590			
Arg	Asp	Glu	Ser	Thr	Ala	Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp		
		595						600				605					
Val	Ala	Met	Ser	Pro	Ile	Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu		
		610					615				620						
Cys	Gly	Asn	Met	Ala	Arg	Glu	Gly	Leu	Arg	Thr	Leu	Val	Val	Ala	Lys		
625					630					635					640		
Lys	Ala	Leu	Thr	Glu	Glu	Gln	Tyr	Gln	Asp	Phe	Glu	Ser	Arg	Tyr	Thr		
				645					650					655			
Gln	Ala	Lys	Leu	Ser	Met	His	Asp	Arg	Ser	Leu	Lys	Val	Ala	Ala	Val		
			660					665					670				
Val	Glu	Ser	Leu	Glu	Arg	Glu	Met	Glu	Leu	Leu	Cys	Leu	Thr	Gly	Val		
		675					680						685				
Glu	Asp	Gln	Leu	Gln	Ala	Asp	Val	Arg	Pro	Thr	Leu	Glu	Met	Leu	Arg		
		690					695				700						
Asn	Ala	Gly	Ile	Lys	Ile	Trp	Met	Leu	Thr	Gly	Asp	Lys	Leu	Glu	Thr		
705					710					715					720		
Ala	Thr	Cys	Ile	Ala	Lys	Ser	Ser	His	Leu	Val	Ser	Arg	Thr	Gln	Asp		
				725					730					735			
Ile	His	Ile	Phe	Arg	Gln	Val	Thr	Ser	Arg	Gly	Glu	Ala	His	Leu	Glu		
			740					745					750				
Leu	Asn	Ala	Phe	Arg	Arg	Lys	His	Asp	Cys	Ala	Leu	Val	Ile	Ser	Gly		
		755					760					765					
Asp	Ser	Leu	Glu	Val	Cys	Leu	Lys	Tyr	Tyr	Glu	His	Glu	Phe	Val	Glu		
		770					775					780					
Leu	Ala	Cys	Gln	Cys	Pro	Ala	Val	Val	Cys	Cys	Arg	Cys	Ser	Pro	Thr		
785					790					795					800		
Gln	Lys	Ala	Arg	Ile	Val	Thr	Leu	Leu	Gln	Gln	His	Thr	Gly	Arg	Arg		
				805					810					815			
Thr	Cys	Ala	Ile	Gly	Asp	Gly	Gly	Asn	Asp	Val	Ser	Met	Ile	Gln	Ala		
			820					825					830				
Ala	Asp	Cys	Gly	Ile	Gly	Ile	Glu	Gly	Lys	Glu	Gly	Lys	Gln	Ala	Ser		
		835					840					845					
Leu	Ala	Ala	Asp	Phe	Ser	Ile	Thr	Gln	Phe	Arg	His	Ile	Gly	Arg	Leu		
							855				860						
Leu	Met	Val	His	Gly	Arg	Asn	Ser	Tyr	Lys	Arg	Ser	Ala	Ala	Leu	Gly		
865					870					875					880		
Gln	Phe	Val	Met	His	Arg	Gly	Leu	Ile	Ile	Ser	Thr	Met	Gln	Ala	Val		
				885					890					895			
Phe	Ser	Ser	Val	Phe	Tyr	Phe	Ala	Ser	Val	Pro	Leu	Tyr	Gln	Gly	Phe		
			900					905					910				
Leu	Met	Val	Gly	Tyr	Ala	Thr	Ile	Tyr	Thr	Met	Phe	Pro	Val	Phe	Ser		
			915					920					925				
Leu	Val	Leu	Asp	Gln	Asp	Val	Lys	Pro	Glu	Met	Ala	Met	Leu	Tyr	Pro		
							935				940						
Glu	Leu	Tyr	Lys	Asp	Leu	Thr	Lys	Gly	Arg	Ser	Leu	Ser	Phe	Lys	Thr		
945					950					955					960		
Phe	Leu	Ile	Trp	Val	Leu	Ile	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Leu	Met		
				965					970					975			

T02E214CP

gaa gca att gat gaa ttt cgg cgt ttt cag cgt gac aag gaa gtg aat 480
 Glu Ala Ile Asp Glu Phe Arg Arg Phe Gln Arg Asp Lys Glu Val Asn
 145 150 155 160

 tca caa cta tat agc aag ctt aca gta aga ggt aaa gtg caa gtt aag 528
 Ser Gln Leu Tyr Ser Lys Leu Thr Val Arg Gly Lys Val Gln Val Lys
 165 170 175

 agt tca gac ata caa gtt gga gac ctc atc ata gtg gaa aag aat caa 576
 Ser Ser Asp Ile Gln Val Gly Asp Leu Ile Ile Val Glu Lys Asn Gln
 180 185 190

 aga att cca tcg gac atg gtg ttt ctt agg act tca gaa aaa gca ggt 624
 Arg Ile Pro Ser Asp Met Val Phe Leu Arg Thr Ser Glu Lys Ala Gly
 195 200 205

 tcg tgt ttt att cga act gat caa cta gat ggt gaa act gac tgg aag 672
 Ser Cys Phe Ile Arg Thr Asp Gln Leu Asp Gly Glu Thr Asp Trp Lys
 210 215 220

 ctg aag gtg gca gtg agc tgc acg caa cag ctg ccg gct ctg ggg gac 720
 Leu Lys Val Ala Val Ser Cys Thr Gln Gln Leu Pro Ala Leu Gly Asp
 225 230 235 240

 ctt ttt tct atc agt gct tat gtt tat gct cag aaa cca caa atg gac 768
 Leu Phe Ser Ile Ser Ala Tyr Val Tyr Ala Gln Lys Pro Gln Met Asp
 245 250 255

 att cac agt ttc gaa ggc aca ttt acc agg gaa gac agt gac ccg ccc 816
 Ile His Ser Phe Glu Gly Thr Phe Thr Arg Glu Asp Ser Asp Pro Pro
 260 265 270

 att cat gaa agt ctc agc ata gaa aat aca ttg tgg gca agc acc att 864
 Ile His Glu Ser Leu Ser Ile Glu Asn Thr Leu Trp Ala Ser Thr Ile
 275 280 285

 gtt gca tca ggt act gta ata ggt gtt gtc att tat acc gga aaa gag 912
 Val Ala Ser Gly Thr Val Ile Gly Val Val Ile Tyr Thr Gly Lys Glu
 290 295 300

 act cga agt gta atg aac aca tcc aat cca aaa aat aag gtt ggt ttg 960
 Thr Arg Ser Val Met Asn Thr Ser Asn Pro Lys Asn Lys Val Gly Leu
 305 310 315 320

 ttg gac ctt gaa ctc aat cgg ctg acg aaa gcg cta ttt ttg gct tta 1008
 Leu Asp Leu Glu Leu Asn Arg Leu Thr Lys Ala Leu Phe Leu Ala Leu
 325 330 335

 gtt gct ctt tcc att gtt atg gta acc tta caa gga ttt gtg ggt cca 1056
 Val Ala Leu Ser Ile Val Met Val Thr Leu Gln Gly Phe Val Gly Pro
 340 345 350

 tgg tac cgc aat ctt ttt cgg ttc ctt ctc ctc ttt tct tac atc att 1104
 Trp Tyr Arg Asn Leu Phe Arg Phe Leu Leu Leu Phe Ser Tyr Ile Ile
 355 360 365

 ccc ata agt ttg cgt gtg aac ttg gac atg ggc aaa gcg gtg tat gga 1152
 Pro Ile Ser Leu Arg Val Asn Leu Asp Met Gly Lys Ala Val Tyr Gly
 370 375 380

 tgg atg atg atg aaa gat gag aac atc cct ggc acg gtc gtt cgg acc 1200

T0416 "E0400"

Trp	Met	Met	Met	Lys	Asp	Glu	Asn	Ile	Pro	Gly	Thr	Val	Val	Arg	Thr		
385					390					395					400		
agc	act	atc	cca	gag	gaa	ctt	ggg	cgc	ctg	gtg	tat	tta	ttg	aca	gac	1248	
Ser	Thr	Ile	Pro	Glu	Glu	Leu	Gly	Arg	Leu	Val	Tyr	Leu	Leu	Thr	Asp		
				405					410					415			
aaa	aca	gga	acc	ctc	acc	cag	aat	gaa	atg	ata	ttt	aag	cgg	ctg	cac	1296	
Lys	Thr	Gly	Thr	Leu	Thr	Gln	Asn	Glu	Met	Ile	Phe	Lys	Arg	Leu	His		
			420					425					430				
ctg	ggc	acc	gtg	tcc	tat	ggc	gcc	gac	acg	atg	gat	gag	atc	cag	agc	1344	
Leu	Gly	Thr	Val	Ser	Tyr	Gly	Ala	Asp	Thr	Met	Asp	Glu	Ile	Gln	Ser		
			435				440						445				
cat	gtc	agg	gac	tcc	tac	tca	cag	atg	cag	tct	caa	gct	ggg	gga	aac	1392	
His	Val	Arg	Asp	Ser	Tyr	Ser	Gln	Met	Gln	Ser	Gln	Ala	Gly	Gly	Asn		
	450					455					460						
aat	act	ggg	tca	act	cca	cta	aga	aaa	gcc	caa	tct	tca	gct	ccc	aaa	1440	
Asn	Thr	Gly	Ser	Thr	Pro	Leu	Arg	Lys	Ala	Gln	Ser	Ser	Ala	Pro	Lys		
465					470				475						480		
gtt	agg	aaa	agt	gtc	agt	agt	cga	atc	cat	gaa	gcc	gtg	aaa	gcc	atc	1488	
Val	Arg	Lys	Ser	Val	Ser	Ser	Arg	Ile	His	Glu	Ala	Val	Lys	Ala	Ile		
				485					490					495			
gtg	ctg	tgt	cac	aac	gtg	acc	ccc	gtg	tat	gag	tct	cgg	gcc	ggc	gtt	1536	
Val	Leu	Cys	His	Asn	Val	Thr	Pro	Val	Tyr	Glu	Ser	Arg	Ala	Gly	Val		
			500					505					510				
aot	gag	gag	act	gag	ttc	gca	gag	gct	gac	caa	gac	ttc	agt	gat	gag	1584	
Thr	Glu	Glu	Thr	Glu	Phe	Ala	Glu	Ala	Asp	Gln	Asp	Phe	Ser	Asp	Glu		
			515				520					525					
aat	cgc	acc	tac	cag	gct	tcc	agc	cgg	gat	gag	gtc	gct	ctg	gtg	cag	1632	
Asn	Arg	Thr	Tyr	Gln	Ala	Ser	Ser	Pro	Asp	Glu	Val	Ala	Leu	Val	Gln		
	530					535					540						
tgg	aca	gag	agt	gtg	ggc	ctc	acg	ctg	gtc	agc	agg	gac	ctc	acc	tcc	1680	
Trp	Thr	Glu	Ser	Val	Gly	Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Thr	Ser		
545					550					555					560		
atg	cag	ctg	aag	acc	ccc	agt	ggc	cag	gtc	ctc	agc	ttc	tgc	att	ctg	1728	
Met	Gln	Leu	Lys	Thr	Pro	Ser	Gly	Gln	Val	Leu	Ser	Phe	Cys	Ile	Leu		
				565					570					575			
cag	ctg	ttt	ccc	ttc	acc	tcc	gag	agc	aag	cgg	atg	ggc	gtc	atc	gtc	1776	
Gln	Leu	Phe	Pro	Phe	Thr	Ser	Glu	Ser	Lys	Arg	Met	Gly	Val	Ile	Val		
			580					585					590				
agg	gat	gaa	tcc	acg	gca	gaa	atc	aca	ttc	tac	atg	aag	ggc	gct	gac	1824	
Arg	Asp	Glu	Ser	Thr	Ala	Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp		
			595				600					605					
gtg	gcc	atg	tct	cct	atc	gtg	cag	tat	aat	gac	tgg	ctg	gaa	gag	gag	1872	
Val	Ala	Met	Ser	Pro	Ile	Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu		
	610					615					620						
tgc	gga	aac	atg	gct	cgc	gaa	gga	ctg	cgg	acc	ctc	gtg	gtt	gca	aag	1920	
Cys	Gly	Asn	Met	Ala	Arg	Glu	Gly	Leu	Arg	Thr	Leu	Val	Val	Ala	Lys		

Total 1920

625	630	635	640	
aag gcg ttg aca	gag gag cag tac cag	gac ttt gag agc cga tac act		1968
Lys Ala Leu Thr	Glu Glu Gln Tyr Gln	Asp Phe Glu Ser Arg Tyr Thr		
	645	650	655	
caa gcc aag ctg	agc atg cac gac agg tcc ctc	aag gtg gcc gcg gta		2016
Gln Ala Lys Leu	Ser Met His Asp Arg Ser	Leu Lys Val Ala Ala Val		
	660	665	670	
gtc gag agc ctg	gag agg gag atg gaa ctg	ctg tgc ctc acc ggc gtg		2064
Val Glu Ser Leu	Glu Arg Glu Met Glu Leu	Leu Cys Leu Thr Gly Val		
	675	680	685	
gag gac cag ctg	cag gca gac gtg cgg ccc acg	ctg gag atg ctg cgc		2112
Glu Asp Gln Leu	Gln Ala Asp Val Arg Pro	Thr Leu Glu Met Leu Arg		
	690	695	700	
aac gcc ggg atc	aag ata tgg atg cta aca	ggc gat aaa ctc gag aca		2160
Asn Ala Gly Ile	Lys Ile Trp Met Leu Thr	Gly Asp Lys Leu Glu Thr		
	705	710	715	720
gct acc tgc att	gcc aaa agt tca cat ctc	gtg tct aga aca caa gat		2208
Ala Thr Cys Ile	Ala Lys Ser Ser His Leu	Val Ser Arg Thr Gln Asp		
	725	730	735	
att cat att ttc	aga cag gta acc agt cgg	gga gag gca cat ttg gag		2256
Ile His Ile Phe	Arg Gln Val Thr Ser Arg	Gly Glu Ala His Leu Glu		
	740	745	750	
ctg aat gca ttt	cga agg aag cat gat tgt	gca cta gtc ata tct ggg		2304
Leu Asn Ala Phe	Arg Arg Lys His Asp Cys	Ala Leu Val Ile Ser Gly		
	755	760	765	
gac tct ctg gag	gtt tgt cta aag tac tac	gag cat gaa ttt gtg gag		2352
Asp Ser Leu Glu	Val Cys Leu Lys Tyr Tyr	Glu His Glu Phe Val Glu		
	770	775	780	
ctg gcc tgc cag	tgc cct gcc gtg gtt tgc	tgc cgc tgc tca ccc acc		2400
Leu Ala Cys Gln	Cys Pro Ala Val Val Cys	Cys Arg Cys Ser Pro Thr		
	785	790	795	800
cag aag gcc cgc	att gtg aca ctg ctg cag	cag cac aca ggg aga cgc		2448
Gln Lys Ala Arg	Ile Val Thr Leu Leu Gln	Gln His Thr Gly Arg Arg		
	805	810	815	
acc tgc gcc atc	ggg gat gga gga aat gat	gtc agc atg att cag gca		2496
Thr Cys Ala Ile	Gly Asp Gly Gly Asn Asp	Val Ser Met Ile Gln Ala		
	820	825	830	
gca gac tgt ggg	att ggg att gag gga aag	gag ggt aaa cag gcc tcg		2544
Ala Asp Cys Gly	Ile Gly Ile Glu Gly Lys	Glu Gly Lys Gln Ala Ser		
	835	840	845	
ctg gcg gcc gac	ttc tcc atc acg cag ttc	cgg cac ata ggc agg ctg		2592
Leu Ala Ala Asp	Phe Ser Ile Thr Gln Phe	Arg His Ile Gly Arg Leu		
	850	855	860	
ctc atg gtg cac	ggg cgg aac agc tac aag	agg tgc gcg gca ctc ggc		2640
Leu Met Val His	Gly Arg Asn Ser Tyr Lys	Arg Ser Ala Ala Leu Gly		
	865	870	875	880

The "GAT" sequence

cag ttc gtc atg cac agg ggc ctt atc atc tcc acc atg cag gct gtg 2688
 Gln Phe Val Met His Arg Gly Leu Ile Ile Ser Thr Met Gln Ala Val
 885 890 895
 ttt tcc tca gtc ttc tac ttc gca tcc gtc cct ttg tat cag ggc ttc 2736
 Phe Ser Ser Val Phe Tyr Phe Ala Ser Val Pro Leu Tyr Gln Gly Phe
 900 905 910
 ctc atg gtg ggg tat gcc acc ata tac acc atg ttc cca gtg ttc tcc 2784
 Leu Met Val Gly Tyr Ala Thr Ile Tyr Thr Met Phe Pro Val Phe Ser
 915 920 925
 tta gtg ctg gac cag gac gtg aag cca gag atg gcg atg ctc tac ccg 2832
 Leu Val Leu Asp Gln Asp Val Lys Pro Glu Met Ala Met Leu Tyr Pro
 930 935 940
 gag ctg tac aag gac ctc acc aag gga aga tcc ttg tcc ttc aaa acc 2880
 Glu Leu Tyr Lys Asp Leu Thr Lys Gly Arg Ser Leu Ser Phe Lys Thr
 945 950 955 960
 ttc ctc atc tgg gtt tta ata agt att tac caa ggc ggc atc ctc atg 2928
 Phe Leu Ile Trp Val Leu Ile Ser Ile Tyr Gln Gly Gly Ile Leu Met
 965 970 975
 tat ggg gcc ctg gtg ctc ttc gag tct gag ttc gtc cac gtg gtg gcc 2976
 Tyr Gly Ala Leu Val Leu Phe Glu Ser Glu Phe Val His Val Val Ala
 980 985 990
 atc tcc ttc acc gca ctg atc ctg acc gag ctg ctg atg gtg gcg ctg 3024
 Ile Ser Phe Thr Ala Leu Ile Leu Thr Glu Leu Leu Met Val Ala Leu
 995 1000 1005
 acc gtc cgc acg tgg cac tgg ctg atg gtg gtg gcc gag ttc ctc agc 3072
 Thr Val Arg Thr Trp His Trp Leu Met Val Val Ala Glu Phe Leu Ser
 1010 1015 1020
 tta ggc tgc tac gtg tcc tca ctc gct ttt ctc aat gaa tat ttt gat 3120
 Leu Gly Cys Tyr Val Ser Ser Leu Ala Phe Leu Asn Glu Tyr Phe Asp
 1025 1030 1035 1040
 gtt gcc ttt atc acc acc gtg acc ttc ctg tgg aaa gtg tcg gcg atc 3168
 Val Ala Phe Ile Thr Thr Val Thr Phe Leu Trp Lys Val Ser Ala Ile
 1045 1050 1055
 acc gtg gtc agc tgc ctc ccg ctg tat gtc ctc aag tac ctg agg cgc 3216
 Thr Val Val Ser Cys Leu Pro Leu Tyr Val Leu Lys Tyr Leu Arg Arg
 1060 1065 1070
 aag tct tct cct ccc agc tac tgc aag ctg gcc tcc taa 3255
 Lys Ser Ser Pro Pro Ser Tyr Cys Lys Leu Ala Ser *
 1075 1080

<210> 25
 <211> 4231
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

TO GET "EAGLE" OUT

<222> (156)...(3443)

<400> 25

```

ggagtcgacc cacgcgtccg cattgagaca atgcctccac aaatacttga tgcaaaattc 60
agtaagacag cacttggtga atcaccatta tagtttctga caaattgttc tcaaaaaggt 120
accagctgga ggatgagtct gcgcatttgg atgaa atg cca cta atg atg tct 173
                               Met Pro Leu Met Met Ser
                               1           5

gaa gaa ggc ttt gag aat gag gaa agt gat tac cac acc tta cca cga 221
Glu Glu Gly Phe Glu Asn Glu Glu Ser Asp Tyr His Thr Leu Pro Arg
                10                15                20

gcc agg ata atg caa agg aaa aga gga ctg gag tgg ttt gtc tgt gat 269
Ala Arg Ile Met Gln Arg Lys Arg Gly Leu Glu Trp Phe Val Cys Asp
                25                30                35

ggc tgg aag ttc ctc tgt acc agt tgc tgt ggt tgg ctg ata aat att 317
Gly Trp Lys Phe Leu Cys Thr Ser Cys Cys Gly Trp Leu Ile Asn Ile
                40                45                50

tgt cga aga aag aaa gag ctg aaa gct cgc aca gta tgg ctt gga tgt 365
Cys Arg Arg Lys Lys Glu Leu Lys Ala Arg Thr Val Trp Leu Gly Cys
                55                60                65                70

cct gaa aag tgt gaa gaa aaa cat ccc agg aat tct ata aaa aat caa 413
Pro Glu Lys Cys Glu Glu Lys His Pro Arg Asn Ser Ile Lys Asn Gln
                75                80                85

aaa tac aat gtg ttt acc ttt ata cct ggg gtt ttg tat gaa caa ttc 461
Lys Tyr Asn Val Phe Thr Phe Ile Pro Gly Val Leu Tyr Glu Gln Phe
                90                95                100

aag ttt ttc ttg aat ctc tat ttt cta gtg ata tcc tgc tca cag ttt 509
Lys Phe Phe Leu Asn Leu Tyr Phe Leu Val Ile Ser Cys Ser Gln Phe
                105                110                115

gta cca gca ttg aaa ata ggc tat ctc tac acc tac tgg gct cct ctg 557
Val Pro Ala Leu Lys Ile Gly Tyr Leu Tyr Thr Tyr Trp Ala Pro Leu
                120                125                130

gga ttt gtc ttg gct gtt act atg aca cgg gaa gca att gat gaa ttt 605
Gly Phe Val Leu Ala Val Thr Met Thr Arg Glu Ala Ile Asp Glu Phe
                135                140                145                150

cgg cgt ttt cag cgt gac aag gaa gtg aat tca caa cta tat agc aag 653
Arg Arg Phe Gln Arg Asp Lys Glu Val Asn Ser Gln Leu Tyr Ser Lys
                155                160                165

ctt aca gta aga ggt aaa gtg caa gtt aag agt tca gac ata caa gtt 701
Leu Thr Val Arg Gly Lys Val Gln Val Lys Ser Ser Asp Ile Gln Val
                170                175                180

gga gac ctc atc ata gtg gaa aag aat caa aga att cca tcg gac atg 749
Gly Asp Leu Ile Ile Val Glu Lys Asn Gln Arg Ile Pro Ser Asp Met
                185                190                195

gtg ttt ctt agg act tca gaa aaa gca ggt tcg tgt ttt att cga act 797
Val Phe Leu Arg Thr Ser Glu Lys Ala Gly Ser Cys Phe Ile Arg Thr
                200                205                210

```

100453-100454

gat caa cta gat ggt gaa act gac tgg aag ctg aag gtg gca gtg agc 845
Asp Gln Leu Asp Gly Glu Thr Asp Trp Lys Leu Lys Val Ala Val Ser
215 220 225 230

tgc acg caa cag ctg ccg gct ctg ggg gac ctt ttt tct atc agt gct 893
Cys Thr Gln Gln Leu Pro Ala Leu Gly Asp Leu Phe Ser Ile Ser Ala
235 240 245

tat gtt tat gct cag aaa cca caa atg gac att cac agt ttc gaa ggc 941
Tyr Val Tyr Ala Gln Lys Pro Gln Met Asp Ile His Ser Phe Glu Gly
250 255 260

aca ttt acc agg gaa gac agt gac ccg ccc att cat gaa agt ctc agc 989
Thr Phe Thr Arg Glu Asp Ser Asp Pro Pro Ile His Glu Ser Leu Ser
265 270 275

ata gaa aat aca ttg tgg gca agc acc att gtt gca tca ggt act gta 1037
Ile Glu Asn Thr Leu Trp Ala Ser Thr Ile Val Ala Ser Gly Thr Val
280 285 290

ata ggt gtt gtc att tat acc gga aaa gag act cga agt gta atg aac 1085
Ile Gly Val Val Ile Tyr Thr Gly Lys Glu Thr Arg Ser Val Met Asn
295 300 305 310

aca tcc aat cca aaa aat aag gtt ggt ttg ttg gac ctt gaa ctc aat 1133
Thr Ser Asn Pro Lys Asn Lys Val Gly Leu Leu Asp Leu Glu Leu Asn
315 320 325

cgg ctg acg aaa gcg cta ttt ttg gct tta gtt gct ctt tcc att gtt 1181
Arg Leu Thr Lys Ala Leu Phe Leu Ala Leu Val Ala Leu Ser Ile Val
330 335 340

atg gta acc tta caa gga ttt gtg ggt cca tgg tac cgc aat ctt ttt 1229
Met Val Thr Leu Gln Gly Phe Val Gly Pro Trp Tyr Arg Asn Leu Phe
345 350 355

cgg ttc ctt ctc ctc ttt tct tac atc att ccc ata agt ttg cgt gtg 1277
Arg Phe Leu Leu Leu Phe Ser Tyr Ile Ile Pro Ile Ser Leu Arg Val
360 365 370

aac ttg gac atg ggc aaa gcg gtg tat gga tgg atg atg atg aaa gat 1325
Asn Leu Asp Met Gly Lys Ala Val Tyr Gly Trp Met Met Met Lys Asp
375 380 385 390

gag aac atc cct ggc acg gtc gtt cgg acc agc act atc cca gag gaa 1373
Glu Asn Ile Pro Gly Thr Val Val Arg Thr Ser Thr Ile Pro Glu Glu
395 400 405

ctt ggg cgc ctg gtg tat tta ttg aca gac aaa aca gga acc ctc acc 1421
Leu Gly Arg Leu Val Tyr Leu Leu Thr Asp Lys Thr Gly Thr Leu Thr
410 415 420

cag aat gaa atg ata ttt aag cgg ctg cac ctg ggc acc gtg tcc tat 1469
Gln Asn Glu Met Ile Phe Lys Arg Leu His Leu Gly Thr Val Ser Tyr
425 430 435

ggc gcc gac acg atg gat gag atc cag agc cat gtc agg gac tcc tac 1517
Gly Ala Asp Thr Met Asp Glu Ile Gln Ser His Val Arg Asp Ser Tyr
440 445 450

tca cag atg cag tct caa gct ggt gga aac aat act ggt tca act cca 1565

T02E1E034007

Ser	Gln	Met	Gln	Ser	Gln	Ala	Gly	Gly	Asn	Asn	Thr	Gly	Ser	Thr	Pro	
455					460					465					470	
cta	aga	aaa	gcc	caa	tct	tca	gct	ccc	aaa	gtt	agg	aaa	agt	gtc	agt	1613
Leu	Arg	Lys	Ala	Gln	Ser	Ser	Ala	Pro	Lys	Val	Arg	Lys	Ser	Val	Ser	
				475					480					485		
agt	cga	atc	cat	gaa	gcc	gtg	aaa	gcc	atc	gtg	ctg	tgt	cac	aac	gtg	1661
Ser	Arg	Ile	His	Glu	Ala	Val	Lys	Ala	Ile	Val	Leu	Cys	His	Asn	Val	
			490					495					500			
acc	ccc	gtg	tat	gag	tct	cgg	gcc	ggc	gtt	act	gag	gag	act	gag	ttc	1709
Thr	Pro	Val	Tyr	Glu	Ser	Arg	Ala	Gly	Val	Thr	Glu	Glu	Thr	Glu	Phe	
		505					510					515				
gca	gag	gct	gac	caa	gac	ttc	agt	gat	gag	aat	cgc	acc	tac	cag	gct	1757
Ala	Glu	Ala	Asp	Gln	Asp	Phe	Ser	Asp	Glu	Asn	Arg	Thr	Tyr	Gln	Ala	
	520					525					530					
tcc	agc	ccg	gat	gag	gtc	gct	ctg	gtg	cag	tgg	aca	gag	agt	gtg	ggc	1805
Ser	Ser	Pro	Asp	Glu	Val	Ala	Leu	Val	Gln	Trp	Thr	Glu	Ser	Val	Gly	
535					540					545					550	
ctc	acg	ctg	gtc	agc	agg	gac	ctc	acc	tcc	atg	cag	ctg	aag	acc	ccc	1853
Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Thr	Ser	Met	Gln	Leu	Lys	Thr	Pro	
				555					560					565		
agt	ggc	cag	gtc	ctc	agc	ttc	tgc	att	ctg	cag	ctg	ttt	ccc	ttc	acc	1901
Ser	Gly	Gln	Val	Leu	Ser	Phe	Cys	Ile	Leu	Gln	Leu	Phe	Pro	Phe	Thr	
			570				575						580			
tcc	gag	agc	aag	cgg	atg	ggc	gtc	atc	gtc	agg	gat	gaa	tcc	acg	gca	1949
Ser	Glu	Ser	Lys	Arg	Met	Gly	Val	Ile	Val	Arg	Asp	Glu	Ser	Thr	Ala	
		585					590					595				
gaa	atc	aca	ttc	tac	atg	aag	ggc	gct	gac	gtg	gcc	atg	tct	cct	atc	1997
Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp	Val	Ala	Met	Ser	Pro	Ile	
	600					605					610					
gtg	cag	tat	aat	gac	tgg	ctg	gaa	gag	gag	tgc	gga	aac	atg	gct	cgc	2045
Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu	Cys	Gly	Asn	Met	Ala	Arg	
615					620					625					630	
gaa	gga	ctg	cgg	acc	ctc	gtg	gtt	gca	aag	aag	gcg	ttg	aca	gag	gag	2093
Glu	Gly	Leu	Arg	Thr	Leu	Val	Val	Ala	Lys	Lys	Ala	Leu	Thr	Glu	Glu	
				635					640					645		
cag	tac	cag	gac	ttt	gag	agc	cga	tac	act	caa	gcc	aag	ctg	agc	atg	2141
Gln	Tyr	Gln	Asp	Phe	Glu	Ser	Arg	Tyr	Thr	Gln	Ala	Lys	Leu	Ser	Met	
			650					655					660			
cac	gac	agg	tcc	ctc	aag	gtg	gcc	gcg	gta	gtc	gag	agc	ctg	gag	agg	2189
His	Asp	Arg	Ser	Leu	Lys	Val	Ala	Ala	Val	Val	Glu	Ser	Leu	Glu	Arg	
		665				670						675				
gag	atg	gaa	ctg	ctg	tgc	ctc	acc	ggc	gtg	gag	gac	cag	ctg	cag	gca	2237
Glu	Met	Glu	Leu	Leu	Cys	Leu	Thr	Gly	Val	Glu	Asp	Gln	Leu	Gln	Ala	
	680					685					690					
gac	gtg	cgg	ccc	acg	ctg	gag	atg	ctg	cgc	aac	gcc	ggg	atc	aag	ata	2285
Asp	Val	Arg	Pro	Thr	Leu	Glu	Met	Leu	Arg	Asn	Ala	Gly	Ile	Lys	Ile	

T0243 634200T

695	700	705	710	
tgg atg cta aca ggc gat aaa ctc gag aca gct acc tgc att gcc aaa				2333
Trp Met Leu Thr Gly Asp Lys Leu Glu Thr Ala Thr Cys Ile Ala Lys	715	720	725	
agt tca cat ctc gtg tct aga aca caa gat att cat att ttc aga cag				2381
Ser Ser His Leu Val Ser Arg Thr Gln Asp Ile His Ile Phe Arg Gln	730	735	740	
gta acc agt cgg gga gag gca cat ttg gag ctg aat gca ttt cga agg				2429
Val Thr Ser Arg Gly Glu Ala His Leu Glu Leu Asn Ala Phe Arg Arg	745	750	755	
aag cat gat tgt gca cta gtc ata tct ggg gac tct ctg gag gtt tgt				2477
Lys His Asp Cys Ala Leu Val Ile Ser Gly Asp Ser Leu Glu Val Cys	760	765	770	
cta aag tac tac gag cat gaa ttt gtg gag ctg gcc tgc cag tgc cct				2525
Leu Lys Tyr Tyr Glu His Glu Phe Val Glu Leu Ala Cys Gln Cys Pro	775	780	785	790
gcc gtg gtt tgc tgc cgc tgc tca ccc acc cag aag gcc cgc att gtg				2573
Ala Val Val Cys Cys Arg Cys Ser Pro Thr Gln Lys Ala Arg Ile Val	795	800	805	
aca ctg ctg cag cag cac aca ggg aga cgc acc tgc gcc atc ggt gat				2621
Thr Leu Leu Gln Gln His Thr Gly Arg Arg Thr Cys Ala Ile Gly Asp	810	815	820	
gga gga aat gat gtc agc atg att cag gca gca gac tgt ggg att ggg				2669
Gly Gly Asn Asp Val Ser Met Ile Gln Ala Ala Asp Cys Gly Ile Gly	825	830	835	
att gag gga aag gag ggt aaa cag gcc tcg ctg gcg gcc gac ttc tcc				2717
Ile Glu Gly Lys Glu Gly Lys Gln Ala Ser Leu Ala Ala Asp Phe Ser	840	845	850	
atc acg cag ttc cgg cac ata ggc agg ctg ctc atg gtg cac ggg cgg				2765
Ile Thr Gln Phe Arg His Ile Gly Arg Leu Leu Met Val His Gly Arg	855	860	865	870
aac agc tac aag agg tcg gcg gca ctc ggc cag ttc gtc atg cac agg				2813
Asn Ser Tyr Lys Arg Ser Ala Ala Leu Gly Gln Phe Val Met His Arg	875	880	885	
ggc ctt atc atc tcc acc atg cag gct gtg ttt tcc tca gtc ttc tac				2861
Gly Leu Ile Ile Ser Thr Met Gln Ala Val Phe Ser Ser Val Phe Tyr	890	895	900	
ttc gca tcc gtc cct ttg tat cag ggc ttc ctc atg gtg ggg tat gcc				2909
Phe Ala Ser Val Pro Leu Tyr Gln Gly Phe Leu Met Val Gly Tyr Ala	905	910	915	
acc ata tac acc atg ttc cca gtg ttc tcc tta gtg ctg gac cag gac				2957
Thr Ile Tyr Thr Met Phe Pro Val Phe Ser Leu Val Leu Asp Gln Asp	920	925	930	
gtg aag cca gag atg gcg atg ctc tac ccg gag ctg tac aag gac ctc				3005
Val Lys Pro Glu Met Ala Met Leu Tyr Pro Glu Leu Tyr Lys Asp Leu	935	940	945	950

100463 E. coli

				485					490					495			
Val	Leu	Cys	His	Asn	Val	Thr	Pro	Val	Tyr	Glu	Ser	Arg	Ala	Gly	Val		
			500						505					510			
Thr	Glu	Glu	Thr	Glu	Phe	Ala	Glu	Ala	Asp	Gln	Asp	Phe	Ser	Asp	Glu		
		515					520					525					
Asn	Arg	Thr	Tyr	Gln	Ala	Ser	Ser	Pro	Asp	Glu	Val	Ala	Leu	Val	Gln		
		530					535					540					
Trp	Thr	Glu	Ser	Val	Gly	Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Thr	Ser		
545					550					555					560		
Met	Gln	Leu	Lys	Thr	Pro	Ser	Gly	Gln	Val	Leu	Ser	Phe	Cys	Ile	Leu		
			565						570					575			
Gln	Leu	Phe	Pro	Phe	Thr	Ser	Glu	Ser	Lys	Arg	Met	Gly	Val	Ile	Val		
			580					585					590				
Arg	Asp	Glu	Ser	Thr	Ala	Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp		
		595					600					605					
Val	Ala	Met	Ser	Pro	Ile	Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu		
		610					615				620						
Cys	Gly	Asn	Met	Ala	Arg	Glu	Gly	Leu	Arg	Thr	Leu	Val	Val	Ala	Lys		
625					630					635					640		
Lys	Ala	Leu	Thr	Glu	Glu	Gln	Tyr	Gln	Asp	Phe	Glu	Ser	Arg	Tyr	Thr		
			645						650					655			
Gln	Ala	Lys	Leu	Ser	Met	His	Asp	Arg	Ser	Leu	Lys	Val	Ala	Ala	Val		
			660					665					670				
Val	Glu	Ser	Leu	Glu	Arg	Glu	Met	Glu	Leu	Leu	Cys	Leu	Thr	Gly	Val		
		675					680					685					
Glu	Asp	Gln	Leu	Gln	Ala	Asp	Val	Arg	Pro	Thr	Leu	Glu	Met	Leu	Arg		
		690					695				700						
Asn	Ala	Gly	Ile	Lys	Ile	Trp	Met	Leu	Thr	Gly	Asp	Lys	Leu	Glu	Thr		
705					710					715					720		
Ala	Thr	Cys	Ile	Ala	Lys	Ser	Ser	His	Leu	Val	Ser	Arg	Thr	Gln	Asp		
			725						730					735			
Ile	His	Ile	Phe	Arg	Gln	Val	Thr	Ser	Arg	Gly	Glu	Ala	His	Leu	Glu		
		740					745					750					
Leu	Asn	Ala	Phe	Arg	Arg	Lys	His	Asp	Cys	Ala	Leu	Val	Ile	Ser	Gly		
		755					760					765					
Asp	Ser	Leu	Glu	Val	Cys	Leu	Lys	Tyr	Tyr	Glu	His	Glu	Phe	Val	Glu		
		770				775					780						
Leu	Ala	Cys	Gln	Cys	Pro	Ala	Val	Val	Cys	Cys	Arg	Cys	Ser	Pro	Thr		
785					790					795					800		
Gln	Lys	Ala	Arg	Ile	Val	Thr	Leu	Leu	Gln	Gln	His	Thr	Gly	Arg	Arg		
			805						810					815			
Thr	Cys	Ala	Ile	Gly	Asp	Gly	Gly	Asn	Asp	Val	Ser	Met	Ile	Gln	Ala		
		820						825					830				
Ala	Asp	Cys	Gly	Ile	Gly	Ile	Glu	Gly	Lys	Glu	Gly	Lys	Gln	Ala	Ser		
		835					840					845					
Leu	Ala	Ala	Asp	Phe	Ser	Ile	Thr	Gln	Phe	Arg	His	Ile	Gly	Arg	Leu		
		850					855				860						
Leu	Met	Val	His	Gly	Arg	Asn	Ser	Tyr	Lys	Arg	Ser	Ala	Ala	Leu	Gly		
865				870					875					880			
Gln	Phe	Val	Met	His	Arg	Gly	Leu	Ile	Ile	Ser	Thr	Met	Gln	Ala	Val		
			885						890					895			
Phe	Ser	Ser	Val	Phe	Tyr	Phe	Ala	Ser	Val	Pro	Leu	Tyr	Gln	Gly	Phe		
			900					905					910				
Leu	Met	Val	Gly	Tyr	Ala	Thr	Ile	Tyr	Thr	Met	Phe	Pro	Val	Phe	Ser		
		915					920						925				
Leu	Val	Leu	Asp	Gln	Asp	Val	Lys	Pro	Glu	Met	Ala	Met	Leu	Tyr	Pro		
		930				935					940						
Glu	Leu	Tyr	Lys	Asp	Leu	Thr	Lys	Gly	Arg	Ser	Leu	Ser	Phe	Lys	Thr		
945					950					955					960		
Phe	Leu	Ile	Trp	Val	Leu	Ile	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Leu	Met		
			965						970					975			

1004-EE-1004

Tyr Gly Ala Leu Val Leu Phe Glu Ser Glu Phe Val His Val Val Ala
 980 985 990
 Ile Ser Phe Thr Ala Leu Ile Leu Thr Glu Leu Leu Met Val Ala Leu
 995 1000 1005
 Thr Val Arg Thr Trp His Trp Leu Met Val Val Ala Glu Phe Leu Ser
 1010 1015 1020
 Leu Gly Cys Tyr Val Ser Ser Leu Ala Phe Leu Asn Glu Tyr Phe Gly
 1025 1030 1035 1040
 Ile Gly Arg Val Ser Phe Gly Ala Phe Leu Asp Val Ala Phe Ile Thr
 1045 1050 1055
 Thr Val Thr Phe Leu Trp Lys Val Ser Ala Ile Thr Val Val Ser Cys
 1060 1065 1070
 Leu Pro Leu Tyr Val Leu Lys Tyr Leu Arg Arg Lys Ser Ser Pro Pro
 1075 1080 1085
 Ser Tyr Cys Lys Leu Ala Ser
 1090 1095

<210> 27
 <211> 3255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(3255)

<400> 27
 atg cca cta atg atg tct gaa gaa ggc ttt gag aat gag gaa agt gat 48
 Met Pro Leu Met Met Ser Glu Glu Gly Phe Glu Asn Glu Glu Ser Asp
 1 5 10 15
 tac cac acc tta cca cga gcc agg ata atg caa agg aaa aga gga ctg 96
 Tyr His Thr Leu Pro Arg Ala Arg Ile Met Gln Arg Lys Arg Gly Leu
 20 25 30
 gag tgg ttt gtc tgt gat ggc tgg aag ttc ctc tgt acc agt tgc tgt 144
 Glu Trp Phe Val Cys Asp Gly Trp Lys Phe Leu Cys Thr Ser Cys Cys
 35 40 45
 ggt tgg ctg ata aat att tgt cga aga aag aaa gag ctg aaa gct cgc 192
 Gly Trp Leu Ile Asn Ile Cys Arg Arg Lys Lys Glu Leu Lys Ala Arg
 50 55 60
 aca gta tgg ctt gga tgt cct gaa aag tgt gaa gaa aaa cat ccc agg 240
 Thr Val Trp Leu Gly Cys Pro Glu Lys Cys Glu Glu Lys His Pro Arg
 65 70 75 80
 aat tct ata aaa aat caa aaa tac aat gtg ttt acc ttt ata cct ggg 288
 Asn Ser Ile Lys Asn Gln Lys Tyr Asn Val Phe Thr Phe Ile Pro Gly
 85 90 95
 gtt ttg tat gaa caa ttc aag ttt ttc ttg aat ctc tat ttt cta gtg 336
 Val Leu Tyr Glu Gln Phe Lys Phe Phe Leu Asn Leu Tyr Phe Leu Val
 100 105 110
 ata tcc tgc tca cag ttt gta cca gca ttg aaa ata ggc tat ctc tac 384
 Ile Ser Cys Ser Gln Phe Val Pro Ala Leu Lys Ile Gly Tyr Leu Tyr
 115 120 125
 acc tac tgg gct cct ctg gga ttt gtc ttg gct gtt act atg aca cgg 432

Thr	Tyr	Trp	Ala	Pro	Leu	Gly	Phe	Val	Leu	Ala	Val	Thr	Met	Thr	Arg	
130						135					140					
gaa	gca	att	gat	gaa	ttt	cgg	cgt	ttt	cag	cgt	gac	aag	gaa	gtg	aat	480
Glu	Ala	Ile	Asp	Glu	Phe	Arg	Arg	Phe	Gln	Arg	Asp	Lys	Glu	Val	Asn	
145					150					155					160	
tca	caa	cta	tat	agc	aag	ctt	aca	gta	aga	ggt	aaa	gtg	caa	gtt	aag	528
Ser	Gln	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Arg	Gly	Lys	Val	Gln	Val	Lys	
				165					170					175		
agt	tca	gac	ata	caa	gtt	gga	gac	ctc	atc	ata	gtg	gaa	aag	aat	caa	576
Ser	Ser	Asp	Ile	Gln	Val	Gly	Asp	Leu	Ile	Ile	Val	Glu	Lys	Asn	Gln	
			180					185					190			
aga	att	cca	tcg	gac	atg	gtg	ttt	ctt	agg	act	tca	gaa	aaa	gca	ggt	624
Arg	Ile	Pro	Ser	Asp	Met	Val	Phe	Leu	Arg	Thr	Ser	Glu	Lys	Ala	Gly	
		195					200					205				
tcg	tgt	ttt	att	cga	act	gat	caa	cta	gat	ggt	gaa	act	gac	tgg	aag	672
Ser	Cys	Phe	Ile	Arg	Thr	Asp	Gln	Leu	Asp	Gly	Glu	Thr	Asp	Trp	Lys	
	210					215					220					
ctg	aag	gtg	gca	gtg	agc	tgc	acg	caa	cag	ctg	ccg	gct	ctg	ggg	gac	720
Leu	Lys	Val	Ala	Val	Ser	Cys	Thr	Gln	Gln	Leu	Pro	Ala	Leu	Gly	Asp	
225					230					235					240	
ctt	ttt	tct	atc	agt	gct	tat	gtt	tat	gct	cag	aaa	cca	caa	atg	gac	768
Leu	Phe	Ser	Ile	Ser	Ala	Tyr	Val	Tyr	Ala	Gln	Lys	Pro	Gln	Met	Asp	
				245					250					255		
att	cac	agt	ttc	gaa	ggc	aca	ttt	acc	agg	gaa	gac	agt	gac	ccg	ccc	816
Ile	His	Ser	Phe	Glu	Gly	Thr	Phe	Thr	Arg	Glu	Asp	Ser	Asp	Pro	Pro	
			260					265					270			
att	cat	gaa	agt	ctc	agc	ata	gaa	aat	aca	ttg	tgg	gca	agc	acc	att	864
Ile	His	Glu	Ser	Leu	Ser	Ile	Glu	Asn	Thr	Leu	Trp	Ala	Ser	Thr	Ile	
		275					280					285				
gtt	gca	tca	ggt	act	gta	ata	ggt	gtt	gtc	att	tat	acc	gga	aaa	gag	912
Val	Ala	Ser	Gly	Thr	Val	Ile	Gly	Val	Val	Ile	Tyr	Thr	Gly	Lys	Glu	
	290					295					300					
act	cga	agt	gta	atg	aac	aca	tcc	aat	cca	aaa	aat	aag	gtt	ggt	ttg	960
Thr	Arg	Ser	Val	Met	Asn	Thr	Ser	Asn	Pro	Lys	Asn	Lys	Val	Gly	Leu	
305					310					315					320	
ttg	gac	ctt	gaa	ctc	aat	cgg	ctg	acg	aaa	gcg	cta	ttt	ttg	gct	tta	1008
Leu	Asp	Leu	Glu	Leu	Asn	Arg	Leu	Thr	Lys	Ala	Leu	Phe	Leu	Ala	Leu	
				325					330					335		
gtt	gct	ctt	tcc	att	gtt	atg	gta	acc	tta	caa	gga	ttt	gtg	ggt	cca	1056
Val	Ala	Leu	Ser	Ile	Val	Met	Val	Thr	Leu	Gln	Gly	Phe	Val	Gly	Pro	
			340					345					350			
tgg	tac	cgc	aat	ctt	ttt	cgg	ttc	ctt	ctc	ctc	ttt	tct	tac	atc	att	1104
Trp	Tyr	Arg	Asn	Leu	Phe	Arg	Phe	Leu	Leu	Leu	Phe	Ser	Tyr	Ile	Ile	
		355					360					365				
ccc	ata	agt	ttg	cgt	gtg	aac	ttg	gac	atg	ggc	aaa	gcg	gtg	tat	gga	1152
Pro	Ile	Ser	Leu	Arg	Val	Asn	Leu	Asp	Met	Gly	Lys	Ala	Val	Tyr	Gly	

T0214CP

[illegible]


```

ctc atg gtg cac ggg cgg aac agc tac aag agg tcg gcg gca ctc ggc 2640
Leu Met Val His Gly Arg Asn Ser Tyr Lys Arg Ser Ala Ala Leu Gly
865                      870                      875                      880

cag ttc gtc atg cac agg ggc ctt atc atc tcc acc atg cag gct gtg 2688
Gln Phe Val Met His Arg Gly Leu Ile Ile Ser Thr Met Gln Ala Val
                        885                      890                      895

ttt tcc tca gtc ttc tac ttc gca tcc gtc cct ttg tat cag ggc ttc 2736
Phe Ser Ser Val Phe Tyr Phe Ala Ser Val Pro Leu Tyr Gln Gly Phe
                        900                      905                      910

ctc atg gtg ggg tat gcc acc ata tac acc atg ttc cca gtg ttc tcc 2784
Leu Met Val Gly Tyr Ala Thr Ile Tyr Thr Met Phe Pro Val Phe Ser
                        915                      920                      925

tta gtg ctg gac cag gac gtg aag cca gag atg gcg atg ctc tac ccg 2832
Leu Val Leu Asp Gln Asp Val Lys Pro Glu Met Ala Met Leu Tyr Pro
                        930                      935                      940

gag ctg tac aag gac ctc acc aag gga aga tcc ttg tcc ttc aaa acc 2880
Glu Leu Tyr Lys Asp Leu Thr Lys Gly Arg Ser Leu Ser Phe Lys Thr
945                      950                      955                      960

ttc ctc atc tgg gtt tta ata agt att tac caa ggc ggc atc ctc atg 2928
Phe Leu Ile Trp Val Leu Ile Ser Ile Tyr Gln Gly Gly Ile Leu Met
                        965                      970                      975

tat ggg gcc ctg gtg ctc ttc gag tct gag ttc gtc cac gtg gtg gcc 2976
Tyr Gly Ala Leu Val Leu Phe Glu Ser Glu Phe Val His Val Val Ala
                        980                      985                      990

atc tcc ttc acc gca ctg atc ctg acc gag ctg ctg atg gtg gcg ctg 3024
Ile Ser Phe Thr Ala Leu Ile Leu Thr Glu Leu Leu Met Val Ala Leu
                        995                      1000                      1005

acc gtc cgc acg tgg cac tgg ctg atg gtg gtg gcc gag ttc ctc agc 3072
Thr Val Arg Thr Trp His Trp Leu Met Val Val Ala Glu Phe Leu Ser
1010                      1015                      1020

tta ggc tgc tac gtg tcc tca ctc gct ttt ctc aat gaa tat ttt gat 3120
Leu Gly Cys Tyr Val Ser Ser Leu Ala Phe Leu Asn Glu Tyr Phe Asp
1025                      1030                      1035                      1040

gtt gcc ttt atc acc acc gtg acc ttc ctg tgg aaa gtg tcg gcg atc 3168
Val Ala Phe Ile Thr Thr Val Thr Phe Leu Trp Lys Val Ser Ala Ile
                        1045                      1050                      1055

acc gtg gtc agc tgc ctc ccg ctg tat gtc ctc aag tac ctg agg cgc 3216
Thr Val Val Ser Cys Leu Pro Leu Tyr Val Leu Lys Tyr Leu Arg Arg
                        1060                      1065                      1070

aag tct tct cct ccc agc tac tgc aag ctg gcc tcc taa 3255
Lys Ser Ser Pro Pro Ser Tyr Cys Lys Leu Ala Ser *
                        1075                      1080

```

<210> 28

<211> 464

<212> PRT

<213> Escherichia coli

2640
2688
2736
2784
2832
2880
2928
2976
3024
3072
3120
3168
3216
3255

<400> 28

Met	Pro	Asp	Ala	Lys	Lys	Gln	Gly	Arg	Ser	Asn	Lys	Ala	Met	Thr	Phe
1				5					10					15	
Phe	Val	Cys	Phe	Leu	Ala	Ala	Leu	Ala	Gly	Leu	Leu	Phe	Gly	Leu	Asp
			20					25					30		
Ile	Gly	Val	Ile	Ala	Gly	Ala	Leu	Pro	Phe	Ile	Ala	Asp	Glu	Phe	Gln
		35					40					45			
Ile	Thr	Ser	His	Thr	Gln	Glu	Trp	Val	Val	Ser	Ser	Met	Met	Phe	Gly
	50					55					60				
Ala	Ala	Val	Gly	Ala	Val	Gly	Ser	Gly	Trp	Leu	Ser	Phe	Lys	Leu	Gly
65					70					75					80
Arg	Lys	Lys	Ser	Leu	Met	Ile	Gly	Ala	Ile	Leu	Phe	Val	Ala	Gly	Ser
				85					90					95	
Leu	Phe	Ser	Ala	Ala	Ala	Pro	Asn	Val	Glu	Val	Leu	Ile	Leu	Ser	Arg
			100					105					110		
Val	Leu	Leu	Gly	Leu	Ala	Val	Gly	Val	Ala	Ser	Tyr	Thr	Ala	Pro	Leu
		115					120					125			
Tyr	Leu	Ser	Glu	Ile	Ala	Pro	Glu	Lys	Ile	Arg	Gly	Ser	Met	Ile	Ser
	130					135					140				
Met	Tyr	Gln	Leu	Met	Ile	Thr	Ile	Gly	Ile	Leu	Gly	Ala	Tyr	Leu	Ser
145					150					155					160
Asp	Thr	Ala	Phe	Ser	Tyr	Thr	Gly	Ala	Trp	Arg	Trp	Met	Leu	Gly	Val
				165					170					175	
Ile	Ile	Ile	Pro	Ala	Ile	Leu	Leu	Leu	Ile	Gly	Val	Phe	Phe	Leu	Pro
			180					185					190		
Asp	Ser	Pro	Arg	Trp	Phe	Ala	Ala	Lys	Arg	Arg	Phe	Val	Asp	Ala	Glu
		195				200						205			
Arg	Val	Leu	Leu	Arg	Leu	Arg	Asp	Thr	Ser	Ala	Glu	Ala	Lys	Arg	Glu
		210				215					220				
Leu	Asp	Glu	Ile	Arg	Glu	Ser	Leu	Gln	Val	Lys	Gln	Ser	Gly	Trp	Ala
225					230					235					240
Leu	Phe	Lys	Glu	Asn	Ser	Asn	Phe	Arg	Arg	Ala	Val	Phe	Leu	Gly	Val
				245					250					255	
Leu	Leu	Gln	Val	Met	Gln	Gln	Phe	Thr	Gly	Met	Asn	Val	Ile	Met	Tyr
			260					265					270		
Tyr	Ala	Pro	Lys	Ile	Phe	Glu	Leu	Ala	Gly	Tyr	Thr	Asn	Thr	Thr	Glu
		275					280					285			
Gln	Met	Trp	Gly	Thr	Val	Ile	Val	Gly	Leu	Thr	Asn	Val	Leu	Ala	Thr
		290				295					300				
Phe	Ile	Ala	Ile	Gly	Leu	Val	Asp	Arg	Trp	Gly	Arg	Lys	Pro	Thr	Leu
305					310					315					320
Thr	Leu	Gly	Phe	Leu	Val	Met	Ala	Ala	Gly	Met	Gly	Val	Leu	Gly	Thr
				325					330					335	
Met	Met	His	Ile	Gly	Ile	His	Ser	Pro	Ser	Ala	Gln	Tyr	Phe	Ala	Ile
			340					345					350		
Ala	Met	Leu	Leu	Met	Phe	Ile	Val	Gly	Phe	Ala	Met	Ser	Ala	Gly	Pro
		355					360					365			
Leu	Ile	Trp	Val	Leu	Cys	Ser	Glu	Ile	Gln	Pro	Leu	Lys	Gly	Arg	Asp
		370				375					380				
Phe	Gly	Ile	Thr	Cys	Ser	Thr	Ala	Thr	Asn	Trp	Ile	Ala	Asn	Met	Ile
385					390					395					400
Val	Gly	Ala	Thr	Phe	Leu	Thr	Met	Leu	Asn	Thr	Leu	Gly	Asn	Ala	Asn
				405					410					415	
Thr	Phe	Trp	Val	Tyr	Ala	Ala	Leu	Asn	Val	Leu	Phe	Ile	Leu	Leu	Thr
			420					425					430		
Leu	Trp	Leu	Val	Pro	Glu	Thr	Lys	His	Val	Ser	Leu	Glu	His	Ile	Glu
		435					440					445			
Arg	Asn	Leu	Met	Lys	Gly	Arg	Lys	Leu	Arg	Glu	Ile	Gly	Ala	His	Asp
		450				455					460				

TOGETHER

370	375	380
Phe Ser Ile Gly Leu Gly Pro Met Pro Trp Leu Val Leu Ser Glu Ile		
385	390	395
Phe Pro Gly Gly Ile Arg Gly Arg Ala Met Ala Leu Thr Ser Ser Met		400
	405	410
Asn Trp Gly Ile Asn Leu Leu Ile Ser Leu Thr Phe Leu Thr Val Asn		415
	420	425
Leu Ile Gly Leu Pro Trp Val Cys Phe Ile Tyr Thr Ile Met Ser Leu		430
	435	440
Ala Ser Leu Leu Phe Val Val Met Phe Ile Pro Glu Thr Lys Gly Cys		445
	450	455
Ser Leu Glu Gln Ile Ser Met Glu Leu Ala Lys Val Asn Tyr Val Lys		460
465	470	475
Asn Asn Ile Cys Phe Met Ser His His Gln Glu Glu Leu Val Pro Lys		480
	485	490
Gln Pro Gln Lys Arg Lys Pro Gln Glu Gln Leu Leu Glu Cys Asn Lys		495
	500	505
Leu Cys Gly Arg Gly Gln Ser Arg Gln Leu Ser Pro Glu Thr		510
	515	520
		525

<210> 31
 <211> 25002
 <212> DNA
 <213> Caenorhabditis elegans

<400> 31

accctgcaat	aggatatcat	tacgatgtaa	gtattcaata	tttatttcaa	atttgtattt	60
tgttgacaaa	ttttcaaata	atgaaatgtg	aatgottcat	gaattcctaa	gctttcgggg	120
cacagaaaag	gagggcgatc	ttcattttta	ctgcaaaaatt	tcaggtacca	tcattgtaag	180
gttgtaaaac	atttttccgt	cgaacaatta	tcacgggaag	aaaattcaca	tgtgctaaac	240
aaaagaaatg	tatggatgga	acagaaccag	ttggtaagtt	tcttttaatt	ttaagggtaa	300
tgtcttattt	tttcagatat	gtcgaagcgt	ctttgcccag	cttgtcgcct	tgcaaaatgt	360
gtggaagtgt	gaatgaatcc	aatggcaatt	caagcagaag	ttaaaactga	tgaaggcaaa	420
gttttaagaa	gtgaagtatt	gaatcaaaga	gaatcgctag	gggttggttc	atctgtaagt	480
tgtttttttt	ttaaaataca	tctattaaat	ttcagttgat	agtaaccgag	gaagatttgt	540
taagcagaat	gattgaaaaa	ttaacatttg	tggaaagtaa	ggttgaacca	ttacatcggt	600
ctggaatgcc	tcctgggttac	agagtaagtt	aatgattttt	ttttaatttg	caagaacttt	660
aattgatttc	aggacataag	aaaattggaa	gaaattcttg	attcaaaacc	agtacttggt	720
gttacggata	ttcccaattt	gaaattctgc	ccttcaccat	gtgcgaatga	aaaaagggtg	780
gtttttttatt	aaaatgagat	tgaaaatttt	cccacttctt	tagaccaaga	cgacatttca	840
ccaactacgt	tcacacaagt	tacctggctt	ctcttgaaat	ttcaaaaatg	tttgaatttt	900
cttcacaact	tgatttgga	tcagaatttc	ttttaatgaa	acacgcgaca	ctaatttggt	960
cgaatatgat	gaatgcattc	ttttcgatta	acgaaatgaa	atcagatatt	cttaggcatt	1020
cggatgggag	catgtcagga	catatgagaa	aattcgatcg	agagaatgat	gtcatgacag	1080
atcatgtcaa	attgatacag	aagacattga	tcactttcct	aaatcataaa	gtcgacaaaa	1140
ttgaatatct	tttattcaaa	gctatttatgc	tttgcaatcc	aggtattttc	cttgccgtca	1200
tatatataat	ttaaaogatt	acttgaaatt	tcagctgtgc	cggattaga	ttcctggaac	1260
caagaaatca	tcgaaaagga	acgaaatcaa	tacgttaaag	ctcttctaaa	ttattgtctc	1320
cttcaacatg	gaaaacttca	aggcccaaca	agatttcgaa	ctattctcgc	aatgggtcca	1380
attatagaga	atcaatcgaa	aaatcaaaaa	gattttccatg	tgtacattaa	agcaaaagcat	1440
ttccagaagc	acaaaaagat	gggaacaacg	ttcagaaaat	gtatcagttg	catgtttgat	1500
caaattatgg	aaacataaat	aatcaatgta	aataaatgac	aatgtttttg	tttaactggt	1560
aatataatct	gttcatcctc	tgtataatat	tctacctcaa	aatacaaaaa	taaacatctc	1620
ataattttatt	ccoctaattc	aaactacaaa	gcatgatgga	aactctatac	attagtcggt	1680
tgtcgtttct	tgtggacgtt	tcattgtggtg	ctgaagttag	gaatttgggc	gatttaccta	1740
cttgatgtaa	cttctaagtt	taacctgaca	tttgcaattt	taagaatttt	ccaagcatta	1800
taaaaaaaat	agttcacact	tttcatgtgc	gagtagatga	taattatgca	agttcaatct	1860
tgcacaggat	taaacctact	agttcacttc	tgattttttat	atattaactt	atcaatgtct	1920
tatttttgaa	gatttttcgt	gtgacagagg	tttcaaaaaa	aagagatatt	caatcagaat	1980
tctaaaagac	aggttggtgaa	acttcaatat	tttcgaatat	accgcacttg	tagtgaattc	2040

agaatataat	tttcaattta	aaaaacacaa	tttttgaagg	tacgcaccaa	tcaogcatct	2100
gaaaatttta	gaaactacac	atatatcagc	aattgatctt	caaaattata	acgacaaaaac	2160
tgaacttcaa	acttttcaaaa	attccagaaa	ttaaaacgac	tgaagtgatt	cttgacagagt	2220
gttgactcaa	agtgaccaat	tggagaccat	actgtttaat	tctttcaaaa	acatttttgat	2280
cgtgcctgt	tacgtataca	aaagaagagt	actgattcat	caaatttgga	atataatccc	2340
accacatgt	aagtgtcgat	agttgttgaa	tcggctgaaa	actttttccg	aaacagaaaag	2400
gagaaagaac	aaacatttga	tagaggcgat	agtcacatca	ttttccactc	tttttctcta	2460
ccatcctatc	tctaatacagt	ctagtcttca	ctaaatcaac	cgttttttata	ttccataaat	2520
tgatccatta	atgtcttcga	aggataggta	gatataattta	tcttgcgttt	attttatttt	2580
tccataatat	tccagtgtat	ctccaccaga	aacttttgaa	gtgtgcatct	cctcaccaga	2640
aatacacaaa	aaagaaataa	tgactccacc	acagaaatca	aaacccaaaaa	gaaatcgacg	2700
gaaaatttac	aaaattcttc	cacaaaatca	atgtccatcg	gtgtgtcaaa	ttttagataaa	2760
tccagcaatt	ggatatcatt	atgaggtaaa	ctacagtata	gtttgtttta	ttgttagaag	2820
tagtgtaaag	gttcaactaga	gctactttaa	agattacgat	tcgatgagtt	attcgattta	2880
ctacatgaac	gctaaactga	gaatatgact	ttaaaaaatg	ttcaactttt	cgggttttgag	2940
aaaaatcaaa	aggcggacac	gaaacacgat	tccacaattt	aagttttcaa	tactattctg	3000
ccttggaaaa	tttatttggg	agaaaagtct	acatacaaac	ccaaaaatca	gtataaaaaat	3060
taagcactct	aaaagagtct	cacgttttag	gtaccatctt	gcaatggatg	caaaacattc	3120
ttccgtcgta	caattatcac	tggccgtaaa	tttaaatgtt	tcaaagttag	taattgtctt	3180
gatggtaatg	acgtaatcgg	tgagttcaat	aagagtctta	atgaaatttt	tttttgatat	3240
ttgcgttttt	gatttctgcc	ttttgatcgg	aaacacattt	ccattcaaat	tttacacaca	3300
ttttccagat	acatcgaagc	gtgtttgtcg	agcatgtoga	tttgaaaaat	gtgtacaagc	3360
gggaatgaat	ccaatggcaa	ttcaagcaga	agcaaagact	gatgaaggag	aagaacttaa	3420
gaaattgatc	gctaaaaagt	ttgaaaacgg	agaaaaatta	aatgatggaa	ccgtattttt	3480
taatgtacat	gacagattga	atcaaatact	tggaaagttg	ataaaaaattg	aaacaaaaatt	3540
ggaaaaagtt	catgataatg	gaatgccaat	gggatttttg	gatcaaagag	atttaagcac	3600
tgcgctctct	tcaaaaagtt	tctataacaa	tatggaaata	ccgtcaatga	gctatactcc	3660
tgttaaaaatt	tcaaaaaaca	ccggattgtg	agtttttttc	aaaagaaaat	tccaaaaatt	3720
tcaaaaaatt	ctgaagtaat	gtttaaatcg	ttttatgagc	attgaagctt	gcctgattgg	3780
ccaaaaataa	acaaaaagct	ccaggcaact	gtaaaaataa	ataaataaag	attataattg	3840
acaaacagta	ttttttacaaa	ttgttgtaaa	ataagttctg	tgcgttttca	ggccaaaacg	3900
aaggagtcca	aactttgttc	attcaagttg	tcttgcatct	atcgaatatt	ccaaaacatt	3960
tgacttttca	agtgcgaattg	acattttcaag	taaagtagct	ttttggaaca	gatttttatct	4020
gaacaatgac	cttatttcgat	tatcttttga	gattatagac	tagcaccatt	tttgcaagta	4080
ttcaaaaatta	atatttagact	tatttcagat	aattctcctt	aaaaatactg	cactatcttg	4140
tgcaaaacttg	acaaatgctt	atacaacatt	cagaaagctg	aaatcagata	cactttttata	4200
cccagatggt	agtattttatg	ggccaccacg	acggaaaaat	ggtccttttg	ttgaaaaaca	4260
acgatcattt	ttacaaaata	cgttgatatc	atttatgact	aacaatgttg	ataaaactga	4320
atatatttta	ctaaaagcaa	tagtactatg	taattccaggt	atgtcataag	taccaataaa	4380
ttaattttca	aataaatatt	acagcaataa	tcgatctacc	ttatgccgat	tcaaaacata	4440
ttcaaagaga	gcgagaggtt	tacgctcagt	gtttgttccg	atattgtcta	ctacaacatg	4500
gtacattaca	cgggcctgca	aggttttctg	ctttattatc	aatattcaat	gtgttggaag	4560
atcaacagaa	ggaacaaaag	gattactatt	tatacatcaa	acttatacat	agtcaaaaaac	4620
acaaggatcc	tgagggtttta	aagaagaaat	gtatttagtgt	aatttatgat	cagattatgg	4680
attagaaaaa	gaaatctaatt	atgatagtga	ataaatagat	tgatgaataa	aaataatttt	4740
gaaatgtaca	tgttttacatt	tttattttgag	tacaatttgt	ttcttgaaac	catattaacc	4800
atgaagtcca	tcaattttat	cttacaaaaa	aaaccactcc	gacttgaaaa	ttaagtgtgg	4860
aatttgccag	tactttcagct	tccttttaaaa	aaaaattcaa	aatgtttaat	tcttttccca	4920
attttctatg	cggattttca	gaacttcaaa	ctattgggaa	catttttgaga	caacccccac	4980
agcttaaaaag	tttttcaaaa	tgttttctccg	ataaaatgca	catataccta	actttttgaat	5040
ataaccoatt	ttctctctga	gtttttatcgt	gattttctgtg	acgaaacact	gaatgcgtac	5100
tgctttttatc	cogattttttc	attgatctcc	attaaaaaca	tcacagtttt	gttggttatta	5160
tctgggtttac	aaagagtcgat	attcagctgt	acatacaagg	gatctaatacg	caacacatta	5220
tgtgcacacg	agcttttgat	cgcaaaacaat	acatcgcggc	taaaaatttt	cgttttctct	5280
acttttctcat	tcattttatac	ttcatgcaac	gtgtgtagat	gagggaagtc	agacgcgagac	5340
ggtacgtaga	ctccaaaagaa	acaaagatgc	gttgatcggg	gcagacgcca	gtcctctctc	5400
taccgttcta	tggtttctgc	gatttttatta	ttccaccttt	tgtgaagttc	gatcacttta	5460
cttttcttgc	ttcaatatca	gaaagatgct	tcctgacttt	attacagtac	catcaacaag	5520
tgaaaagtat	gttttaattctc	cagaattggt	ttgtttgcat	agatgatggg	aaatcaataa	5580
ccttctgttc	atgtgacgcg	cggtatcata	tttctcttct	tttttcagat	gtctttctcc	5640
ggaattgttg	ctaccaaata	tggatgagaa	cttgggaagat	tcaaaaaccaa	gcgtgagttt	5700

tccctatttcg	gaaaaatata	ctttctaaaa	aaatatTTaa	aaacaatcaa	aaagttaaag	5760
tattaatttat	atatctcaaa	acgatatatc	tcaaaaacgt	tatatTCgaa	tttcagTctt	5820
taaaatatca	aaaggcgatg	atgagccgag	gaacatgtcc	atcaaattgt	aaagtctgta	5880
ggcactcagc	tactggatat	cactatgatg	ttccatcttg	taatggatgc	aaaacatttt	5940
ttcgacgatc	aattctggat	ggaagaaaaat	atacatgcct	gaagatgaga	aaatgtttga	6000
gtggaactga	acctgttggg	atgctttaat	tttctcacta	attcaagatt	tcactatccc	6060
tatcatatac	ttcaaaccat	ttcagacttg	tctagggcga	tgtgtcgagc	atgccgattt	6120
gagaaatgtg	tagaagctgg	aatgaatcca	tctgcaatac	aagccgacat	gaaaaccact	6180
gacggtgagc	tgttgagaaa	agaaattatg	ataaagcaga	agacagccgt	tgattttttg	6240
aatactccac	aggtatat	caaaaaataat	tgcaacaatg	ataatcactg	attattttcag	6300
gttattatga	gttttgaaga	taaagtgcaa	ggaataattg	gcaagctgac	agtaatggaa	6360
ttgaagatag	aaccattgta	tacaggagga	ttgcctccag	gcaatagagt	atgatgcttt	6420
tcctgtaaac	tggtaacctt	ataattcagg	atatcaggaa	attggacgag	ttgattgatg	6480
ctccactgat	tctcagctat	gacgaaaattc	caaatTTtaa	gtattgtccg	agtgtagacg	6540
aattgaccgg	agagtgaagt	tttattcaga	aaaatcaatg	attccataaa	attatttttc	6600
agaataaagc	ccagtggagc	ttgctacata	cattgcccgt	acctagctag	tatagaatat	6660
tcaaaaatgt	ttgactttgc	tcataaaata	gatgttgcta	gcaaagcaac	tctgataaaa	6720
catgcaacaa	ttatgtgcgc	agatatcatg	acagctttct	tctcttacta	tcaacgtaaa	6780
tccgatcgac	tgattcatcc	aaatggaaatg	tttgaggagc	cacaaaaata	caggtgaaac	6840
acttcagtaa	atatgttttt	gaaaaatgat	tttgcttgag	atatggtgaa	gccggtacaa	6900
aatatcaagc	ttcaatgcaa	agaactctgg	caacagtgtc	ccgacatgaa	cttaaatcgaa	6960
ttgaatatat	gctactcaaa	gctatttgtc	tttgcgaatc	aggtatgacc	aaaaattttg	7020
aatcaaaaaac	acaaaaacat	caatttcaat	acaggagtcc	atgaaaataa	tatcttttaa	7080
taacacgatt	tgattttccag	cagtctctag	tctttctatt	tcggtacaac	aaataattgg	7140
aaaagaacgt	gaagaatatg	ttcgaactct	acttacatac	tgtctttctca	attatggttc	7200
tgttcatgga	ccatcaagat	tttctgccct	tcttgctatt	atgtcagttc	ttgaaagtca	7260
acagaagaat	gcaaaggact	ttcattttatt	ggctaaagcg	acaatactga	aagatgcagt	7320
tagatacaca	cgaattagca	atcttttacga	acaaatcatg	gagtcgtaaa	gattagaaat	7380
tgttgaaatt	aggatatTTg	ggtaactcgaa	gtcttttatt	ttattacttt	caatttatgt	7440
tatatttcta	tttatatata	catttgagaa	atacaaaagaa	atcagagaaa	atcatcagaa	7500
ttgttgcaatt	ggttctagcg	ggtattgtaa	ataaaatggt	atttttccgt	ttcgaatctt	7560
ctctacataa	agcttttctga	tcagcacata	aagtgagaat	agaagtTTgg	attaaattac	7620
aacctgaatc	cgttatccgc	aatcagttta	accgcacgt	aaagacaatc	agcagtgaga	7680
tcaggagtca	cgggcacott	ttcgaaatct	gggtctccatt	taccagttct	cacttgaaca	7740
cctcgcattc	cacaagcttg	agcaccgcct	acgtccgaca	tcaaatcgtc	gccaaccatt	7800
acaatctgga	aattagaaaa	tgaagtcaca	aagattttgt	tccaacataa	gaatggaaat	7860
tgaaattccg	atgtataatt	gttttactta	cttcttctgg	tttcataccc	aatgcattca	7920
ttccttgctc	gaaatagaac	cggttgggt	ttccaatgtt	caaaacctca	caattagttg	7980
agaacttgag	agcagcgaca	aaagcgccga	cttcaatgca	cggaccatca	actcgttgga	8040
agaactttct	aaaaatagaaa	agggaaatgt	gttagagaga	acaggaaaca	attattacc	8100
attgccatt	gttatgagaa	gcggttttagg	catgtcgatg	agaattcggga	aagctctgtt	8160
gattcgatcg	aatgagaaac	cttcttcaac	ttcaccatc	acaacacaat	tcggagatga	8220
ggtgtcgatt	ccatcgaaat	attcaagcac	atcttgagag	gaaaaagaac	tgattgttgt	8280
cagagaatta	aagaatcaaa	taccgtctct	gacaaacaga	tgtgggCGaa	gcttgttctc	8340
tcgacaatat	tgtgcaacca	ctggagctgg	agttatgacg	tcttcctctc	gaacactgaa	8400
aataaaaaact	attataattc	caataagtag	tgggtgattt	gaaagctgcc	tatttgacat	8460
tattaatttt	tacattattc	ggtaacactt	tttttctaaa	tttgttctat	cagacttcag	8520
taggacattt	tggttggttt	tgaattgatg	actgatcaac	agaaatattt	tctgaatctc	8580
aaaaaatcaa	tggtcgggag	agtgaatttt	tttttctgat	ttcttccatc	ggaaaacatg	8640
caaaaattgg	gtaaaatttg	atttctacaa	aaaccgtgaa	ataactctca	aacttacttg	8700
attccgagtc	tttgaagtct	ccgagcaaca	tttctgtttg	aatttccctt	tgcatgtcta	8760
agaaatttta	ccttcgagtg	ttgatacaaa	ctgtaaatat	tttcaatatt	atgtatctat	8820
ttttgcattt	tacaatattt	ttcttatcta	atgcaccgtt	gttctaggtg	cacatgcacg	8880
caaatgttta	ccttgagggc	attttttata	aacagttttc	caaaaatttg	tggaaatttt	8940
ttcggattga	gaacaaaata	caggacatgt	aaaacgattt	gacataaaaag	tgataaaactt	9000
gaaaaatgag	gatacatgat	ttgtatctac	catttttatt	aacaaaaaag	agttgaagtt	9060
tttattagct	agaaaaatca	ttaaaaaact	tacaaattaa	ccgcttcagc	tgatttttga	9120
acagcaactc	catcggattt	ataaatacta	ttatacaaaa	ctcccgttat	atcgagcagg	9180
aaccatttaa	ccgtctttcc	atttgacatt	cttcgaccct	aaagtttcaa	tatgaaattt	9240
cataatcctg	aaaccaagac	caaagttcag	gaaaccagca	aaagctataa	catagaacaa	9300
aaacagaaaa	gatagaatga	aaatcttgag	atagctatgg	aaaaggaaga	gaggaaaggg	9360

tctttctctc	tttctttcca	tgcgggggca	atatgggcag	aaaggggtccg	tttagatggt	9420
cttctctctg	ctcactgcat	gtgcacccag	tacgtcttct	tcacttctct	cacctctctc	9480
actcctttct	tgttccacta	tctcttcaat	acacatgtcc	agctgcctat	tggaccttct	9540
gttttcaagg	tgttgtcaca	acttttgagc	tatgaaacta	ctttgatgct	aattagatat	9600
gatttagtaa	tatgtatttt	gtttcatagc	tcacacagaa	aatgtatatc	atgagaaaca	9660
tcagagagat	ttagcaatgg	atccgtaatg	tatctttaat	gaactcaaga	tattcatatt	9720
ttaaaacgtg	tttactactca	aaataaatga	atattgtaag	aaaacactga	atcgcatacc	9780
caaaagcctc	caaactttca	aaagatgtag	agtaaccata	caaaacaata	ggaagagttc	9840
gaaatgtgca	gtcacgcgcg	catttcttgt	gtctctaagg	tgtgaattac	gcaaacacag	9900
agacggcaga	ttgcgggtatg	tccggtcgaga	atgatgaatt	acgatcaaga	caagaaaaga	9960
agaagaagaa	ggaaagacga	accagagatt	ttcgactgca	gtagctgagg	aacaattgta	10020
gaagaataact	cggcgtcact	ttataaataa	atgaaacaaa	atcttgatta	aaagagaagc	10080
tagaagggtca	cgtttaatact	atgaggttat	gcacttgaaa	ttatgcaata	tttcaaattg	10140
cacagaaaaa	accaacaggt	aataaaatca	atcaagtctg	aaaatgttgc	tctagaaatg	10200
tgtatcgtac	aatgaagcgt	gtatctctga	atcaaaaacg	tttagactgt	gacaattctt	10260
tccggaatcc	aataagaaca	aagtgtggaa	aagggatgca	ccgagctgaa	aattttattga	10320
actgtagttt	gaggaactca	atcaagacga	accaaaccatc	attcatgcga	agaaacatca	10380
tttaatttta	gaaactataa	aaaaaagggt	aaaacattta	actggcattc	agagacaatt	10440
cttaaaaactt	tgatggcgca	aaacaacaag	acgtcatcca	cagaagaaac	tgtgccctac	10500
atcttcaaat	agatcggaca	tcatctatct	acaagtattc	tttctttttc	attctcttgt	10560
ccctctccat	cagccctcct	tgatagtctt	ttttcacatt	ctcaccttct	tttttgctgt	10620
ctattttactt	ttatgattgc	cgaccaataa	aatatctcta	ctcaatttca	aactccttat	10680
cgatttaatc	catatgtact	atacttttaa	agacagatta	tgcgtgaggc	gaatgtgaca	10740
tagtctagaa	ttccggaaat	tgtgcgcaaa	attcttagaa	acatatgtag	ttgagtcgca	10800
tttttcgaat	ccagttttta	tttcagcggc	tgttttattt	cagcggctgt	tttatgactg	10860
cattttttaca	agctgctaatt	tgcgaatttc	cacgataacg	gtttgggttg	cacgtgtttc	10920
ccaataaatt	tgtaaagcatt	ttacataatg	caccaatttt	tccctccaca	catcatttcc	10980
gaatttgatt	tttttttctt	aaattacttg	aacatattat	cgaaaaaaat	tgaaactggt	11040
cccatactca	caaaacatca	ttcaatagta	ttagattcag	aaaactgcct	acaaattgat	11100
tttttaacca	ttggttttca	tgaactatct	ttcaacaatt	cagatgaact	ttttttaaaa	11160
ttcaaagtgc	tattatgtta	ttacaattag	aagaaattaa	aaattcaaat	tatacaattt	11220
aagtttggtc	ctatcacggg	ttttaaatga	atttcttgaa	aacgcgcggc	aaaagcttag	11280
caaactgtct	attgaactta	cccttactat	taatcattga	aattttcaaa	tgcgtatatt	11340
taaaaaaaca	gaacggtatg	gattctcatg	ataagacagt	tccttaatat	ctcgtagcaa	11400
aaaaatcgac	ccatctcttt	gccccttgct	tcatttctgc	cgctttcttc	gtgccaggaa	11460
ggtaggcatt	ctcgtgaacc	gacggtctga	gtttgagtgt	tttcctctta	aaatgttcga	11520
ttatttatagg	tgcgcagaca	taaatattat	ttgttaatat	ttcatgggtg	cgaaccacca	11580
atcttttttc	tttctacagg	tggttttaata	ttcgtttcct	ttgtaaattt	tcccatcggc	11640
aggaattggc	ataacctgat	tttttacagt	agaaacacat	atctagaaga	ttaagatctt	11700
caattgtcca	tctcgtttta	aactgtcatt	tctccggttc	tttttggttt	ttggtggcct	11760
tttaccgggt	ttgttaacgt	ttcccgaat	gatataaatt	tttgagcttg	tcacttaatt	11820
tatcaagcgg	cgaccaaaga	caaatacaca	ccgcagaaga	aaagtttgta	aagagaaatg	11880
gaagtgtact	atatgtacat	atataaaatg	gaatgaatag	tcgcatcaca	ttgacgggtga	11940
aagtacatgc	ggtgatgcct	tccaggacat	acggacacac	tttccttctc	caatttcatt	12000
gattaatttg	tattgttata	ttotgaattc	caggttttca	agacgaacat	tgtgaatcat	12060
tttcatcaca	ttgttctggt	acaaataaaa	tgtattttcca	agttttcccg	cacatttaca	12120
tttttgcttc	actacgtggt	tagcacgtta	tgcgataaga	ggagaagtgg	ctgtaaaatg	12180
gtttcgcact	cccttttttc	tctcccacaa	tcattgcacg	gtttctatga	ccttttcgaa	12240
ctacattcct	tcttttttca	tttgagggtt	tgatactgat	atagtttgta	gggtaccgcg	12300
ttattgtaac	tctaactggt	atatccattg	tcattgattc	atattatctg	gggtatttcc	12360
cttctatttg	gcgaagtcta	catttctcgt	aaactgtaca	aaataacgtt	taaaagtctt	12420
ttgaatactg	aaaataataa	aacgggttga	acaatccaac	ttattttcca	atttttcaaaa	12480
actagccgat	cattttttgtg	aaataaaaact	attttctgct	tagtatcgaa	taaaacatct	12540
taacggtaaa	aatgagtttt	ttaaaacact	tctttttaaac	cttttttgga	tttatttgaa	12600
ttttggcttt	gaaatagtct	ttattccgga	aattttcatat	aatctcaagg	gcaaaatacat	12660
tttgaaccgt	gttcaaagtt	attttaaaat	gcatttcggt	tgaatcactg	agattttcaa	12720
aaattcaatg	agtcataata	catggagcaa	caaatctata	agaatgtcca	cttgcttttg	12780
ttgttctttt	gttttcaaac	gttttgagata	taggctgtta	ttttggccga	caacaacttc	12840
agaatgtatt	ttatgtttga	gttttaaatg	tgttactgaa	aacaaataaa	atgacagatt	12900
aatatatctc	ttggtaaaaa	tttaattaatt	ttgttactac	tttctgttcc	tgaaaagcct	12960
gaaaaatcag	accattttttt	gcagtgtctt	tgttaatgat	aaaaaccgac	atgcacactg	13020

```

accatcaaac cgattattat gaattaataa tttaatccga cagtttcctg tttctgttca 13080
tttcatctca cgaatgcttc aatttttcatt ttttttttcc gtgtctctta atacgtttta 13140
tttattacga gttcaagtaa caacgtttca atgaactctc atttagtttg aaaattaaaa 13200
tattttaagtt ctaacatttt gaagagttaa cgatggtgag aaacaaagtg gcaccagttg 13260
aagatggagc caatattcaa agaaacttcg agcctccgcc accatataca actccaacgg 13320
attcacctga agacaagatt cgatcaaatt caactgcaac aaccgcatct caaccagaat 13380
ttcaaggatg ttggactatt gttgtagttg ccatttttatt catcatcaat cttctcaatt 13440
atatggatcg gtatacgatt gcaggttagt tgacagtaac tattttacct ccttggtaca 13500
atattcaaaa cacaattcat gtaaccatgt gacagttttc cgtgcaataa aatttagtag 13560
agcctccaaa actataaaca acaaaaggta gaaagatgaa aatggccgga aaacgacatg 13620
agagagtatc ttgtttgaac ttgtcatcat tagaagataa gaatttacgt aatgggtgag 13680
tacaataact atgggacaaa catcattttt tgatctaaac ggagcattaa aaaatatgtg 13740
catgtcaaat ttgaattagt atgtgtggaa cttttcctac tgcaataata taacgttttc 13800
aacaaaaaaa acattaaaaa cattattcgt agaggaaatt agcatttaaa aaccaataaa 13860
attttttagga gtccttaatg atgtacaaac ctactacaat attagtgatg cttgggctgg 13920
actgattcaa acaacgttca tgggtgttctt cattattttc tctccaattt gcggtttcct 13980
aggagatcgt tacaatcgaa aatggatttt tggtgttggg attgcgattt ggggtgtctgc 14040
agtgtttgct tccactttta ttccatctaa tgtgagtttt tgactctaata catactattt 14100
cttcaatcaa cttcattttc agcaattctg gttgttccct ttattccgcg gaattgttg 14160
aatcggagaa gcactctatg caattatctc cccaactgtt attgctgata tgttactg 14220
agtgtccgt tccagaatgc ttatggtctt ctactttgcg attccctttg gatgtggtct 14280
gggatttgta gttggatctg ctgtggctag ttggacagga cattggcaat ggggagtacg 14340
agtgactgga gttctcggaa tcgttttgtc cttgcttatt atcgtgtttg tttagaagac 14400
agaacgtgga aaagctgaac gtgaaaaggg agaaattgct gcactctacag aagcaacaag 14460
ttatttgga gatatgaagg atttgttttc aaagtgaagt tctttcaatt ttatttaaaa 14520
agcaaccttt catatttcag tgcaacatat gtgacaagca gtctcggtta tactgcaact 14580
gttttcatgg tcggaactct cgcttggtgg gctccaatta caattcaata tgcagattct 14640
gctagaagga acggaacaat tacagaagat cagaaagcaa acattaactt ggtattcggt 14700
gcactcactt gtgttggtgg cgttcttggt gttgtctatt gtacattggt ttcaaagtga 14760
aatattgtcg ttgaagatta gaaaaatata catctttttt ttagatgtgg tctcgtggag 14820
ttggtccttt taagcacatt caaacgttc gtgcagatgc tcttgctctg gctatcggag 14880
cagcaatttg cattccaaca ctcatctctg ctattcaaaa cattgagagc aacatgaatt 14940
ttgcttggtt gtgtaaaatt tggactatga aacatttcaa attcgctttt ttttagggaa 15000
tgttatttat ttgcattgtc gccagtagtt ttaactgggc taaaaatgtc gatctgttac 15060
tggtaaagtt cactcgatat tgaaacaaat tcccaaataa atgttttttg cagagtgtgg 15120
tagttcctca gagaagaagt tcagcctcat catggcaaat ttttaattct catatgtttg 15180
gagatgcttc tggctcctac attctgggat tgatatcaga tgcaatcaga ggcaatgaag 15240
atacggcaca ggctcattat aaatcattgg tcacctcatt ttggttgtgt gttggaactt 15300
tgggtttgtc agttattcta tttggaatat cagcaataac agttgtaaaa gataaagcca 15360
gattcaacga aattatgtgt aagtttcaga ctttttatag cttggcactg aatcaaaaata 15420
ttcatttgca gtggcacaag ctaacaagga caacacatca agcgggacac ttccaattga 15480
agacagaaac acagaagacg aaactgggtc cgaagttcaa catatgtaat tctaattatt 15540
tagtaaaagt ggttgcctaa cccctcttcc cctacatatt acatttttct cacagtttat 15600
tgccgggtctg ctcttttttt tgtatttttg tatcccccat cagtcaatca ttgcataaa 15660
ttttgcgttt ttattgccaa atctttttgta catttcggaa tattcgtgct gtcagagaaa 15720
atcaatgata gcagttaacg tgattcttta tgcttttcat agtgtttttg aaaaatatga 15780
aaacaagttt ctacttgga cttttttatg gagcctcctt gttgtgtggc ggacaaatga 15840
caacagaagc tgggtaaaaa gtaagtttta ttcaaacat actatacttc gccttccac 15900
ctctcgcccg gaaatgtttt cggaaaagta tagtaaaagt cagttgaagt gttaacatgg 15960
taacaaaaat ggcatacaaa actaccggtc aggcgcgagg aggcgaataa agaggcgagc 16020
atgaatcacc aatgtggaac gccgttattt tggtttattg tagaaatatt actttcgaac 16080
aaaatcgtga cgcacaacaa aaataacttt tgcgttagct tgcaagtttca atttttaaaa 16140
ttttccatgg ttgtccaaat ttctgcatag caaagtactt gtcacgtttt tcaacataag 16200
aacagttttc agaaaccaac tttgattcat ttttcattta cataatttca gatacaattg 16260
aaatctgcaa tattgtaaga ttcatatcag ttccattatt tcattcatct ccagtttaatt 16320
ggcttttatt atttactaca tcttcagcat tttcttttat tgctcaaagt tggtttctaa 16380
aaaatcaaaa gtttttaaac tgaccaattc agaaaaagaa tttactggat tcacattaat 16440
gatcgctctt catttgattc aatattttct catcacagga ttaagtgtgaa tgacatattg 16500
gaatttagga aaacaattat ttaattttat tgtttggcca gatgattctc gtcaactaat 16560
cattcagttg gcaatgattt tgtctactgc aactatgttc tgtcaogtat ttatcagtat 16620
ttgggtcaaa ctttcagaga ttatcaatat aagtttgttt tttttacatt gtttctctga 16680

```


aacagtatta	tatatTTTTgc	cttcagattg	gtttctagtt	tctaccatcg	ttcatcctgc	16740
tattagtTTTc	tacatcTTTc	cgagattTtca	acatgtTcat	atgttgactg	tttggTTTTc	16800
TTTTcttatg	atttcagTTa	aatttaaatca	gaagatgtTc	attaaagtTc	tcggagtTct	16860
tttcattgTt	ctatactcca	gcTTTTtgga	atcctgggaa	ttatatTTTT	tggatttgaa	16920
gtcactTTTT	aaaataaaat	atTTattcTa	acaagtgtTt	acgtagtaag	cattaactTtA	16980
aatatggtga	aatggaaaat	atggtgctTa	aaaaacatca	aaatgaacac	agactaccga	17040
atttgataat	gacactTcgg	taatcctTct	caaaaattTt	tattactgtt	ttaaatgtTa	17100
gaataaaaagg	ctcaaaaaca	aacctccaac	tattagcagc	cggagaagt	aattaaattg	17160
aaacaaattt	agggccgctg	caagcctTtT	ctttataaat	tttgaacaat	tataaattca	17220
gtctttgaaa	gccaatTTga	gttttattTa	gcagtatata	tttttagata	gtcggcattt	17280
gaatctatca	acaattTTta	tcatcatcat	catgtTtTatc	atcaacagta	cctccactgt	17340
ttcgtacaat	atcatcatat	cgtaaataag	ttctTctgtc	agcattTgat	ggacctggac	17400
gaacacaatc	cgcataTcga	agacgatgaa	atctTgtagc	ataggtTgga	ggatctctga	17460
aattgtTcca	atTTtctTcc	agtgtTattc	cgaaagaatc	gtaccggtaa	tgtaaaatTt	17520
atTTtctcaa	aattcctTca	aaacaagctt	cagtgtcaga	atTTtagaaga	agtatctgaa	17580
tcaaacaac	ctaatacagat	gaaactTTta	actTcatacc	caattaaac	accaagattg	17640
gcttaaactg	aatccaggcc	accagaatag	tcccatattg	acaatatcgg	attgtTTtaaa	17700
gaaaatcttg	aaatgatcac	gagatcctTg	ttcaaaaatcg	tttctTcctg	ggttatcgag	17760
atgaaaagtt	tcagaatcat	gtccagattc	atagaataact	ttcaaatatg	atgcggcgtc	17820
tgttccagca	ccatctTtTg	cacaagtctc	tatgactaca	tccagagac	gaccgtcatc	17880
tacaaaactg	aataaattgcc	actTattTga	atTTgaatac	aacaattTtT	agaaaagttt	17940
tattatgatt	gttgtTcatt	tcagcatTgt	atgcgtgatt	ttaaacgatt	ttcttgattg	18000
acacattagt	tgaactcaaa	gttaagattTa	aaaataaatat	taaaactacat	cattgtTcac	18060
aactTcctgg	aaagtTtTtag	tgaggTtcat	attcgaatat	tctctTcaac	cccatTTtTta	18120
aaagtTgact	tgtgtTtTta	ttgtTtTacc	tttctgatca	tttctatcat	tgaaattTgga	18180
agtcattTtca	ctTTtctTcc	cacagctcat	agttacaaaa	acaagagtga	ctgaaattTt	18240
aaaaactact	tgtggtTtTca	gtTTtTtatt	tattTtatga	atccagttag	tcgaaaaaaa	18300
aacaatcaaa	ttaatTccat	gcaacccaaa	atattTtTaa	gttctTggta	tttatgcagt	18360
ttTtaaaact	gagaatcaaa	agTtaaaaata	attgtTtTta	actTacgatg	aacaacagtt	18420
tcattagtTg	gagaaaaattg	tgcaaaaaacg	aatagtaacta	gtaagcagta	tattaaaaat	18480
gagtggaaaca	ttTtggggag	ttggtgaaaa	atttatagga	agagatgaaa	gacactTtTg	18540
gttctggaat	ctTctctTga	cgacaactaa	aaatocataca	gcaattgaaa	tgatcgattg	18600
atgattgatg	gatgagtTg	atcatatgct	tgctcaaaat	actTtcaaa	cgaaaaaaa	18660
acacaaggga	aacatgagtt	ctaaattTtT	gatcggaaca	gatggtagaa	attgaaatgt	18720
ttggattcgt	catcggtaaa	atgaatataa	acattTtatta	gtgcaataa	acaatcaaaa	18780
tttaatatTa	aacaagatga	aaaatatgac	ctgattTtTt	gaaattattc	tggTtTgtgaa	18840
aaaatattTg	tatgattata	caaatcgaaa	tagttTcaaac	tctcaaaatg	atgtctctcc	18900
ggaatctcgt	gtattTtTcac	gagtTtTcagt	tctTtTcaaaa	aacgtgcaa	atattTtTctt	18960
ataaaaacaaa	tagtctTtTga	ctaaatcaaa	gattaccgtg	atatgagatc	ttaaaagtag	19020
cattggTtat	aagctattTaa	tatgattaat	acgagatact	gtaattgtag	atttagttTa	19080
gcttcatata	tctctaattt	aactTtTtTaa	gcctcgagtt	aagtattTtTa	catttgaaca	19140
attgtgtaat	caaaacgcaa	tctgtacat	aattattTtT	agcgtgtat	tttctctcat	19200
caatcaaaaa	atttaattTt	taaaaataat	ttgattTacc	gagcatctga	acagaagcaa	19260
ggacacgtga	gtTtgctgat	tttgctgata	agaaatcaat	tatttaggtg	cattggTgat	19320
cttcattctt	tttctaaact	tatcagaaaa	aatatattct	ctattTtTtaa	catttattgt	19380
gttctacatg	ttctacatgg	ttTtgTatat	tcgtaacaat	ttTtTaaagta	gaaaaaaaata	19440
tatactgata	atcagcaaaa	actagtTtTt	gtTcacattt	tgatatcatc	actTtTtTtat	19500
tatattcaac	tagagtTtTaa	aatattTaat	ttattgattc	ttatcgatat	ttTtgactat	19560
tgattcccgT	gtTgatcgct	ttgtgataat	aaaattTtTg	gaacaaatta	gccaatcgTg	19620
cattTtTtTgt	catcaattTca	atattatctg	acgattcctg	ttcctgttag	ttgcaaaatc	19680
atgaacaagt	atcactTtTt	ctatatTtTta	tttcatattt	ttcccgTcat	gaaacgttat	19740
gtTtTgctc	atataaaatc	aaaaatgaac	aaaaaagtgg	tgTtTgactt	gaaaacaaga	19800
ttTtTtaggac	agaaggTcgg	atgggaaaag	gtTtTcgTtT	gacggacatc	acacaaaaaa	19860
gtatcacacc	gcacctcat	ctattTtactt	tgTtgataga	atggaaaaac	attcgactga	19920
aaatgaatac	agagTaaagt	tattTtTtTcca	aaaatgtTtT	aaataatgat	tcaattTtTta	19980
ggtgtataag	gaacgatggt	ttattctTtT	ggcgactact	gcattgattt	gctcaaatat	20040
ttgtgtgagt	aatggaaat	tggtattTtT	atatttagat	tggcgtgaat	ttTgtctaaga	20100
agtccgatgt	ttTtTcaaaa	ttcaaataca	ttacaaaagta	gtgccaaaat	taaacattTt	20160
ttagattTtT	tgTtTtagct	gaaaagTtTg	acgaggtgtt	cataaattTta	aagagTtTtT	20220
gaaaacaaac	ctTtaattTat	gatgtTtctg	cattTtctTac	aatTtTtTgag	gtaattTtaat	20280
agaagacgag	cctgccacaa	aacggtTtTta	ccagattTtT	caaactTtTaa	caattattTta	20340

ctggatttaa	aataaaacat	attaatgttt	tttctgcagc	aatgggtgag	tttctcggct	20400
caaatcgacc	aaacaaatat	gtttttctgt	ggcccaaagt	aatataagaa	ttgttcagca	20460
gccttcctat	ctaatacaat	ctatcaggtt	agatttttca	attttgatcg	gtataattta	20520
ttatatattt	tttagatagt	tcagtaatt	gtgagcatta	taggaatgta	ttttgcaaca	20580
gtttttggaa	cacttccaac	tgtatgtttc	ttcttctaata	ttacagtttt	ctaattttaca	20640
cgtcttctag	ctccgtctct	cagcagtttt	caatattggt	ggtgcagcaa	tccgactcat	20700
tgcgtcactt	ccaagccttc	aaaacttttt	ctggagacag	tttttaatga	ttattggaac	20760
tagcattgcc	gcggctgctc	aaatgtattt	cgtcgtcttc	tcgaaaattg	cggaaagttg	20820
gttttatcca	agacatcgag	cttctgcaaa	tgttgcatgt	tcaaatagtc	ttgagttagg	20880
agttgtactt	ggaactgttt	taccatcaat	tattgtacca	gottctttta	caaaaagacat	20940
tgtcagttcc	tggacatttt	ttcttttggg	tagttatgtc	tctgtcatga	ttaaacaact	21000
atattacaat	ttcagaattc	aataatagca	gttgtagta	taattccatt	atttttatta	21060
tttgttctat	gccgtcgatc	ggttccaaaa	acgccaccat	cagcctcctc	gcaacatgag	21120
tcaagtggtc	ctgtgacatc	tggtagtttt	aaatgtttta	agtaagcccg	tacttagctg	21180
tttaattttt	attcttctga	tagttctcag	ggatcgtcag	tttctcattc	aaatattcgt	21240
ttattcaatt	aattttgcaa	ttgcaaatgg	cctcatttat	acttctaatt	ccatcaacta	21300
tagagggtat	aatttgaaag	ggtacgtcta	gtaagggttt	ctgctaggta	caagaaatcc	21360
tactctgtca	agtaggcagg	cattttttaga	cctgcctagg	aggtttaaac	tcaagacagc	21420
cctttgcgta	taattatttt	gttcagggtat	ccaatagcaa	tcgccacgat	ggtctgcatg	21480
ttttcagcct	atttcgtagg	agtaattgca	gatagaacaa	gaaagttcaa	agttagtttc	21540
aaaaaatcta	atcttatctg	atatccattt	ttctagttga	tcgcaataat	aaacgcactt	21600
gttgtagccg	tttgtagctg	ggtacttcgt	ctggtaaggc	tttttcaaaa	taacattaaa	21660
tttattcatt	aatgctttta	gtattttaata	aaaacttata	cgggatggta	tgattcagta	21720
attgtttgta	cacttttaag	cattatcagt	aagttatttt	aattttgctt	atttagaata	21780
tattttcaaa	aattcagtg	cctgttgtgc	tatacataca	ccgattggaa	atgagatggg	21840
agttgagaca	acttaccag	ttcaagaatc	aattttctaca	ggagttttga	atactttcgg	21900
gtgagccttt	ggttcttttt	acggcgaaaa	aaagtgtgat	ataccgcgtt	ttttgggtct	21960
cgcagcgaat	ttgtattttcg	gtttgtgctt	ttctgatatt	aattttatac	gagttttatt	22020
caaaacgaaa	cgttaaaaaa	tttttcagtc	aagcttggtt	attctgctta	tattttatta	22080
tgtattcttt	acaagaatca	aattgggttt	acaagaacaa	ccgtaaagga	ggaagctggg	22140
aatgtaagtt	tcttttttaa	tttttaaac	atgtttcaac	taacgcggtc	acttacaagc	22200
ctgtgtagct	ttagttttcta	actaattttc	aaataattta	aagttttttt	tctaatagta	22260
aataaaaaata	taaatattac	gggaacacta	aatactgaaa	gtgcgtattg	cacaacatat	22320
ttgacgcgaa	aaatgatttg	tagcgtagcg	aaaactacag	caacttttta	gatgactacc	22380
gtagaactgg	tttacggaac	tcgtgtttca	atcgataaaa	tattaaaaga	aaacacaaaa	22440
atgacaaaac	aataaaaaaa	aaacttttaa	aaaaattgaa	tattgttgct	acaattcgca	22500
caaataacttg	tttcgtaact	agagccccac	ggcccgagaa	gtggtacctg	tacgcaattt	22560
gtctaccgta	cacctggacg	tttgggcgcg	ttttttctcaa	aaacggctgg	tccagttttt	22620
ttgtgatgca	tataaaaaat	gttcgaaaat	aaattcaaaa	ttttttggac	caaagctttt	22680
tccttaaaaac	gagcccaaac	ctggctaaac	tgcaattatc	aatagagcgc	gtttacactg	22740
atgtaccctt	tgcggggtcg	tgagcccgta	aaccgacacc	agcactaagt	acagaagtca	22800
ttaaaataat	tgttttaatg	ttcgctacga	tatatttccg	ggtcaaatat	gttgcgcaat	22860
acgcattttc	aaaacgtagt	gttctctgta	attatgtttt	cattttctgct	tcaaaaaacta	22920
aatattttat	attacagtag	cccttgactt	ctgggcagga	atgtctattc	taaactttat	22980
tgtggctgta	atattcttga	gaccccgata	taaccgttta	caaatggaag	aagaagctca	23040
aaatacacgg	gaagcaattc	gagattcagt	gtataacaatt	tgtaaagtaat	gaactgcttt	23100
tattttatcaa	tgatgtaaat	aataaaaaaa	tgaatttgct	gaaaaaaaata	aagtcatgag	23160
aaacaggaaa	tgcgatatga	gacaatgggt	aaaaaagatt	gggactagtt	gaaactgggt	23220
gcaaatgaac	tgggtgaagtc	tagaaacata	atataaacat	gtttgttggt	caaaaataatt	23280
tcaaattgag	actatggtac	atatgatttt	ttaagtgaaga	aaatacaatt	cctctaactt	23340
cttaagtaca	aaatgctata	aaatgcaaag	taaatgcttg	ctactatcgc	atttcgatata	23400
ccgacgcagc	cgttcgagct	gtaacaggtt	cctcattttc	taatgccaat	ttggcatttt	23460
ccagttctag	acgacgatata	ctgtaattga	taaaattatt	tattgagttt	tgataaacgt	23520
ttataccgtg	gtctcaaaaa	gaacagtgat	aagatgacag	atacaattga	gagccacat	23580
gttacatcga	gagcaactga	aaaatattca	tttacttcta	ttttgaagat	gataaaaactt	23640
acatttccaa	gattgtgcata	agaacaagt	caacttttct	gtgtaatttt	gtgcaaatgg	23700
aataatgaac	atgaaaagcg	atccgaatat	aacaagaaca	cctgatgaog	ttgcttccat	23760
tactgggaat	gtcgtctcaa	caccaagttc	cactccaatc	gggaattgag	gtattgaaaa	23820
ggcacctgaa	gaaatatagg	aattttgtta	tacaattaaa	tttaaaaaat	ccttaccgag	23880
acatccacaa	agagtgtaaa	cgattatgct	atcaaagagc	ccagtccgtg	gttgatttag	23940
gaactgcaag	tgtagccttt	ttagattaaa	aaaatccata	gaggaaattt	agacataattg	24000

```

acacaatttt tttcgaagac cctggtagaa gaattttaac tcaccattct caatgtaatg 24060
actgaacatg aaaatccaac agtacaaact ctgattatct cctaaatttt aaaattatat 24120
tttttttttc tgattcatac cgaccactca ccttgaactt gcgtgttttg tcggcaatat 24180
gaccagcgag cagtgatgtt aacgtgccaa cgattgcaca cacggcagtt ggatatctga 24240
aaaataaatg aattactcat atgcttctag aactctgcaa agttgttacc cagccatctc 24300
ataaccttga tctttgagtg gaccatcgag gaaaatcatt agactccaca gaagcgaaaa 24360
cgaaatgca aagagagtca tttggatgaa aaattgagca ttactgaaat taaagtatct 24420
aaagtttttg gcgtgatact aaaaacctac aaaatacatt gaagaataga tttaaagaaa 24480
ccaatgttgt tctgatgagc agcagaagaa gctgatgggtg gagtgggtgg cagtttagtt 24540
cgaacgaata gtgctagaac aaatgggaac aaggctagac attccattcc aagagtctga 24600
aaatatgaat tgtcaatgat aattaaattg agtactaaca aatgtgaaga acatccaact 24660
attcgaatca atagtcttat tgtgaccaa aagaatggat ggcacaattg ttccgagggc 24720
aacaccgga ggatttgctg aaattgatag gaattactta cgaacattaa aattccacta 24780
accaacaaaa gaaagtacat ttgcaattgc tctctgatca ccaggaacc agcattcagc 24840
aatttttgat ggaagaacta aaaagaatgc ttgtgctgaa gcagcgataa acgatcctgc 24900
atgaagaaga cattcacgaa caaaatgtga ttttatgaaa ggaatcgagg caatcatccg 24960
aatcgatgct ccaattacat ttaaagtgtg accaagaaga cc 25002

```

<210> 32

<211> 1237

<212> PRT

<213> Rattus norvegicus

<400> 32

```

Met Ala Arg Ala Lys Leu Pro Arg Ser Pro Ser Glu Gly Lys Ala Gly
 1          5          10          15
Pro Gly Asp Thr Pro Ala Gly Ser Ala Ala Pro Glu Glu Pro His Gly
 20          25          30
Leu Ser Pro Leu Leu Pro Thr Arg Gly Gly Gly Ser Val Gly Ser Asp
 35          40          45
Val Gly Gln Arg Leu His Val Glu Asp Phe Ser Leu Asp Ser Ser Leu
 50          55          60
Ser Gln Val Gln Val Glu Phe Tyr Val Asn Glu Asn Thr Phe Lys Glu
 65          70          75          80
Arg Leu Lys Leu Phe Phe Ile Lys Asn Gln Arg Ser Ser Leu Arg Ile
 85          90          95
Arg Leu Phe Asn Phe Ser Leu Lys Leu Leu Thr Cys Leu Leu Tyr Ile
 100         105         110
Val Arg Val Leu Leu Asp Asn Pro Asp Gln Gly Ile Gly Cys Trp Gly
 115         120         125
Cys Thr Lys Tyr Asn Tyr Thr Phe Asn Gly Ser Ser Ser Glu Phe His
 130         135         140
Trp Ala Pro Ile Leu Trp Val Glu Arg Lys Met Ala Leu Trp Val Ile
 145         150         155         160
Gln Val Ile Val Ala Thr Ile Ser Phe Leu Glu Thr Met Leu Leu Ile
 165         170         175
Tyr Leu Ser Tyr Lys Gly Asn Ile Trp Glu Gln Ile Phe His Val Ser
 180         185         190
Phe Val Leu Glu Met Ile Asn Thr Leu Pro Phe Ile Ile Thr Val Phe
 195         200         205
Trp Pro Pro Leu Arg Asn Leu Phe Ile Pro Val Phe Leu Asn Cys Trp
 210         215         220
Leu Ala Lys His Ala Leu Glu Asn Met Ile Asn Asp Phe His Arg Ala
 225         230         235         240
Ile Leu Arg Thr Gln Ser Ala Met Phe Asn Gln Val Leu Ile Leu Phe
 245         250         255
Cys Thr Leu Leu Cys Leu Val Phe Thr Gly Thr Cys Gly Ile Gln His
 260         265         270
Leu Glu Arg Ala Gly Gly Asn Leu Asn Leu Leu Thr Ser Phe Tyr Phe
 275         280         285

```

Cys	Ile	Val	Thr	Phe	Ser	Thr	Val	Gly	Phe	Gly	Asp	Val	Thr	Pro	Lys
290						295					300				
Ile	Trp	Pro	Ser	Gln	Leu	Leu	Val	Val	Ile	Leu	Ile	Cys	Val	Thr	Leu
305					310					315					320
Val	Val	Leu	Pro	Leu	Gln	Phe	Glu	Glu	Leu	Val	Tyr	Leu	Trp	Met	Glu
				325					330					335	
Arg	Gln	Lys	Ser	Gly	Gly	Asn	Tyr	Ser	Arg	His	Arg	Ala	Arg	Thr	Glu
			340					345					350		
Lys	His	Val	Val	Leu	Cys	Val	Ser	Ser	Leu	Lys	Ile	Asp	Leu	Leu	Met
		355					360					365			
Asp	Phe	Leu	Asn	Glu	Phe	Tyr	Ala	His	Pro	Arg	Leu	Gln	Asp	Tyr	Tyr
		370				375					380				
Val	Val	Ile	Leu	Cys	Pro	Ser	Glu	Met	Asp	Val	Gln	Val	Arg	Arg	Val
385					390					395					400
Leu	Gln	Ile	Pro	Leu	Trp	Ser	Gln	Arg	Val	Ile	Tyr	Leu	Gln	Gly	Ser
				405					410					415	
Ala	Leu	Lys	Asp	Gln	Asp	Leu	Met	Arg	Ala	Lys	Met	Asp	Asn	Gly	Glu
			420					425					430		
Ala	Cys	Phe	Ile	Leu	Ser	Ser	Arg	Asn	Glu	Val	Asp	Arg	Thr	Ala	Ala
		435					440					445			
Asp	His	Gln	Thr	Ile	Leu	Arg	Ala	Trp	Ala	Val	Lys	Asp	Phe	Ala	Pro
		450				455					460				
Asn	Cys	Pro	Leu	Tyr	Val	Gln	Ile	Leu	Lys	Pro	Glu	Asn	Lys	Phe	His
465					470					475					480
Val	Lys	Phe	Ala	Asp	His	Val	Val	Cys	Glu	Glu	Glu	Cys	Lys	Tyr	Ala
				485					490					495	
Met	Leu	Ala	Leu	Asn	Cys	Ile	Cys	Pro	Ala	Thr	Ser	Thr	Leu	Ile	Thr
			500					505					510		
Leu	Leu	Val	His	Thr	Ser	Arg	Gly	Gln	Glu	Gly	Gln	Glu	Ser	Pro	Glu
		515					520					525			
Gln	Trp	Gln	Arg	Met	Tyr	Gly	Arg	Cys	Ser	Gly	Asn	Glu	Val	Tyr	His
	530					535					540				
Ile	Arg	Met	Gly	Asp	Ser	Lys	Phe	Phe	Arg	Glu	Tyr	Glu	Gly	Lys	Ser
545					550					555					560
Phe	Thr	Tyr	Ala	Ala	Phe	His	Ala	His	Lys	Lys	Tyr	Gly	Val	Cys	Leu
				565					570					575	
Ile	Gly	Leu	Lys	Arg	Glu	Glu	Asn	Lys	Ser	Ile	Leu	Leu	Asn	Pro	Gly
			580					585					590		
Pro	Arg	His	Ile	Leu	Ala	Ala	Ser	Asp	Thr	Cys	Phe	Tyr	Ile	Asn	Ile
		595					600					605			
Thr	Lys	Glu	Glu	Asn	Ser	Ala	Phe	Ile	Phe	Lys	Gln	Glu	Glu	Lys	Gln
		610				615					620				
Asn	Arg	Arg	Gly	Leu	Ala	Gly	Gln	Ala	Leu	Tyr	Glu	Gly	Pro	Ser	Arg
625					630					635					640
Leu	Pro	Val	His	Ser	Ile	Ile	Ala	Ser	Met	Val	Ala	Met	Asp	Leu	Gln
				645					650					655	
Asn	Thr	Asp	Cys	Arg	Pro	Ser	Gln	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly
			660					665					670		
Lys	Leu	Thr	Leu	Pro	Thr	Glu	Asn	Gly	Ser	Gly	Ser	Arg	Arg	Pro	Ser
		675				680						685			
Ile	Ala	Pro	Val	Leu	Glu	Leu	Ala	Asp	Ser	Ser	Ala	Leu	Leu	Pro	Cys
		690				695					700				
Asp	Leu	Leu	Ser	Asp	Gln	Ser	Glu	Asp	Glu	Val	Thr	Pro	Ser	Asp	Asp
705					710					715					720
Glu	Gly	Leu	Ser	Val	Glu	Tyr	Val	Lys	Gly	Tyr	Pro	Pro	Asn	Ser	
				725					730					735	
Pro	Tyr	Ile	Gly	Ser	Ser	Pro	Thr	Leu	Cys	His	Leu	Leu	Pro	Val	Lys
			740					745					750		
Ala	Pro	Phe	Cys	Cys	Leu	Arg	Leu	Asp	Lys	Gly	Cys	Lys	His	Asn	Ser
		755					760					765			
Tyr	Glu	Asp	Ala	Lys	Ala	Tyr	Gly	Phe	Lys	Asn	Lys	Leu	Ile	Ile	Val

Total = 69900

<210> 33
 <211> 638
 <212> PRT
 <213> Rattus norvegicus

<400> 33

Met	Gly	Lys	Ile	Glu	Asn	Asn	Glu	Arg	Val	Ile	Leu	Asn	Val	Gly	Gly
1				5					10					15	
Thr	Arg	His	Glu	Thr	Tyr	Arg	Ser	Thr	Leu	Lys	Thr	Leu	Pro	Gly	Thr
			20					25					30		
Arg	Leu	Ala	Leu	Leu	Ala	Ser	Ser	Glu	Pro	Gln	Gly	Asp	Cys	Leu	Thr
		35					40					45			
Ala	Ala	Gly	Asp	Lys	Leu	Gln	Pro	Leu	Pro	Pro	Pro	Leu	Ser	Pro	Pro
		50				55					60				
Pro	Arg	Pro	Pro	Pro	Leu	Ser	Pro	Val	Pro	Ser	Gly	Cys	Phe	Glu	Gly
65					70				75						80
Gly	Ala	Gly	Asn	Cys	Ser	Ser	His	Gly	Gly	Asn	Gly	Ser	Asp	His	Pro
			85						90					95	
Gly	Gly	Gly	Arg	Glu	Phe	Phe	Phe	Asp	Arg	His	Pro	Gly	Val	Phe	Ala
			100					105					110		
Tyr	Val	Leu	Asn	Tyr	Tyr	Arg	Thr	Gly	Lys	Leu	His	Cys	Pro	Ala	Asp
		115					120					125			
Val	Cys	Gly	Pro	Leu	Phe	Glu	Glu	Glu	Leu	Ala	Phe	Trp	Gly	Ile	Asp
		130				135					140				
Glu	Thr	Asp	Val	Glu	Pro	Cys	Cys	Trp	Met	Thr	Tyr	Arg	Gln	His	Arg
145					150					155					160
Asp	Ala	Glu	Glu	Ala	Leu	Asp	Ile	Phe	Glu	Thr	Pro	Asp	Leu	Ile	Gly
				165					170					175	
Gly	Asp	Pro	Gly	Asp	Asp	Glu	Asp	Leu	Gly	Gly	Lys	Arg	Leu	Gly	Ile
			180					185					190		
Glu	Asp	Ala	Ala	Gly	Leu	Gly	Gly	Pro	Asp	Gly	Lys	Ser	Gly	Arg	Trp
		195				200						205			
Arg	Lys	Leu	Gln	Pro	Arg	Met	Trp	Ala	Leu	Phe	Glu	Asp	Pro	Tyr	Ser
		210				215					220				
Ser	Arg	Ala	Ala	Arg	Phe	Ile	Ala	Phe	Ala	Ser	Leu	Phe	Phe	Ile	Leu
225					230					235					240
Val	Ser	Ile	Thr	Thr	Phe	Cys	Leu	Glu	Thr	His	Glu	Ala	Phe	Asn	Ile
				245					250					255	
Val	Lys	Asn	Lys	Thr	Glu	Pro	Val	Ile	Asn	Gly	Thr	Ser	Ala	Val	Leu
			260					265					270		
Gln	Tyr	Glu	Ile	Glu	Thr	Asp	Pro	Ala	Leu	Thr	Tyr	Val	Glu	Gly	Val
		275				280						285			
Cys	Val	Val	Trp	Phe	Thr	Phe	Glu	Phe	Leu	Val	Arg	Ile	Val	Phe	Ser
		290				295					300				
Pro	Asn	Lys	Leu	Glu	Phe	Ile	Lys	Asn	Leu	Leu	Asn	Ile	Ile	Asp	Phe
305					310					315					320
Val	Ala	Ile	Leu	Pro	Phe	Tyr	Leu	Glu	Val	Gly	Leu	Ser	Gly	Leu	Ser
			325						330					335	
Ser	Lys	Ala	Ala	Lys	Asp	Val	Leu	Gly	Phe	Leu	Arg	Val	Val	Arg	Phe
		340						345					350		
Val	Arg	Ile	Leu	Arg	Ile	Phe	Lys	Leu	Thr	Arg	His	Phe	Val	Gly	Leu
		355				360						365			
Arg	Val	Leu	Gly	His	Thr	Leu	Arg	Ala	Ser	Thr	Asn	Glu	Phe	Leu	Leu
		370				375					380				
Leu	Ile	Ile	Phe	Leu	Ala	Leu	Gly	Val	Leu	Ile	Phe	Ala	Thr	Met	Ile
385					390					395					400
Tyr	Tyr	Ala	Glu	Arg	Val	Gly	Ala	Gln	Pro	Asn	Asp	Pro	Ser	Ala	Ser
			405						410					415	
Glu	His	Thr	Gln	Phe	Lys	Asn	Ile	Pro	Ile	Gly	Phe	Trp	Trp	Ala	Val
			420					425					430		
Val	Thr	Met	Thr	Thr	Leu	Gly	Tyr	Gly	Asp	Met	Tyr	Pro	Gln	Thr	Trp

Trp 638

435 440 445
 Ser Gly Met Leu Val Gly Ala Leu Cys Ala Leu Ala Gly Val Leu Thr
 450 455 460
 Ile Ala Met Pro Val Pro Val Ile Val Asn Asn Phe Gly Met Tyr Tyr
 465 470 475 480
 Ser Leu Ala Met Ala Lys Gln Lys Leu Pro Arg Lys Arg Lys Lys His
 485 490 495
 Ile Pro Pro Ala Pro Leu Ala Ser Ser Pro Thr Phe Cys Lys Thr Glu
 500 505 510
 Leu Asn Met Ala Cys Asn Ser Thr Gln Ser Asp Thr Cys Leu Gly Lys
 515 520 525
 Glu Asn Arg Leu Leu Glu His Asn Arg Ser Val Leu Ser Gly Asp Asp
 530 535 540
 Ser Thr Gly Ser Glu Pro Pro Leu Ser Pro Pro Glu Arg Leu Pro Ile
 545 550 555 560
 Arg Arg Ser Ser Thr Arg Asp Lys Asn Arg Arg Gly Glu Thr Cys Phe
 565 570 575
 Leu Leu Thr Thr Gly Asp Tyr Thr Cys Ala Ser Asp Gly Gly Ile Arg
 580 585 590
 Lys Gly Tyr Glu Lys Ser Arg Ser Leu Asn Asn Ile Ala Gly Leu Ala
 595 600 605
 Gly Asn Ala Leu Arg Leu Ser Pro Val Thr Ser Pro Tyr Asn Ser Pro
 610 615 620
 Cys Pro Leu Arg Arg Ser Arg Ser Pro Ile Pro Ser Ile Leu
 625 630 635

<210> 34

<211> 1187

<212> PRT

<213> Mus musculus

<400> 34

Met Asp Cys Ser Leu Leu Arg Thr Leu Val Arg Arg Tyr Cys Ala Gly
 1 5 10 15
 Glu Glu Asn Trp Val Asp Ser Arg Thr Ile Tyr Val Gly His Lys Glu
 20 25 30
 Pro Pro Pro Gly Ala Glu Ala Tyr Ile Pro Gln Arg Tyr Pro Asp Asn
 35 40 45
 Arg Ile Val Ser Ser Lys Tyr Thr Phe Trp Asn Phe Ile Pro Lys Asn
 50 55 60
 Leu Phe Glu Gln Phe Arg Arg Ile Ala Asn Phe Tyr Phe Leu Ile Ile
 65 70 75 80
 Phe Leu Val Gln Leu Ile Ile Asp Thr Pro Thr Ser Pro Val Thr Ser
 85 90 95
 Gly Leu Pro Leu Phe Phe Val Ile Thr Val Thr Ala Ile Lys Gln Gly
 100 105 110
 Tyr Glu Asp Trp Leu Arg His Lys Ala Asp Asn Ala Met Asn Gln Cys
 115 120 125
 Pro Val His Phe Ile Gln His Gly Lys Leu Val Arg Lys Gln Ser Arg
 130 135 140
 Lys Leu Arg Val Gly Asp Ile Val Met Val Lys Glu Asp Glu Thr Phe
 145 150 155 160
 Pro Cys Asp Leu Ile Phe Leu Ser Ser Asn Arg Ala Asp Gly Thr Cys
 165 170 175
 His Val Thr Thr Ala Ser Leu Asp Gly Glu Ser Ser His Lys Thr His
 180 185 190
 Tyr Ala Val Gln Asp Thr Lys Gly Phe His Thr Glu Ala Asp Val Asp
 195 200 205
 Ser Leu His Ala Thr Ile Glu Cys Glu Gln Pro Gln Pro Asp Leu Tyr
 210 215 220

102
 202
 302
 402
 502
 602
 702
 802
 902
 1002
 1102
 1202
 1302
 1402
 1502
 1602
 1702
 1802
 1902
 2002
 2102
 2202
 2302
 2402
 2502
 2602
 2702
 2802
 2902
 3002
 3102
 3202
 3302
 3402
 3502
 3602
 3702
 3802
 3902
 4002
 4102
 4202
 4302
 4402
 4502
 4602
 4702
 4802
 4902
 5002
 5102
 5202
 5302
 5402
 5502
 5602
 5702
 5802
 5902
 6002
 6102
 6202
 6302
 6402
 6502
 6602
 6702
 6802
 6902
 7002
 7102
 7202
 7302
 7402
 7502
 7602
 7702
 7802
 7902
 8002
 8102
 8202
 8302
 8402
 8502
 8602
 8702
 8802
 8902
 9002
 9102
 9202
 9302
 9402
 9502
 9602
 9702
 9802
 9902
 10002

Total Residues

Lys	Phe	Val	Gly	Arg	Ile	Asn	Val	Tyr	Asn	Asp	Leu	Asn	Asp	Pro	Val	225	230	235	240
Val	Arg	Pro	Leu	Gly	Ser	Glu	Asn	Leu	Leu	Leu	Arg	Gly	Ala	Thr	Leu	245	250	255	
Lys	Asn	Thr	Glu	Lys	Ile	Phe	Gly	Val	Ala	Ile	Tyr	Thr	Gly	Met	Glu	260	265	270	
Thr	Lys	Met	Ala	Leu	Asn	Tyr	Gln	Ser	Lys	Ser	Gln	Lys	Arg	Ser	Ala	275	280	285	
Val	Glu	Lys	Ser	Met	Asn	Thr	Phe	Leu	Ile	Val	Tyr	Leu	Cys	Ile	Leu	290	295	300	
Val	Ser	Lys	Ala	Leu	Ile	Asn	Thr	Val	Leu	Lys	Tyr	Val	Trp	Gln	Ser	305	310	315	320
Glu	Pro	Phe	Arg	Asp	Glu	Pro	Trp	Tyr	Asn	Glu	Lys	Thr	Glu	Ser	Glu	325	330	335	
Arg	Gln	Arg	Asn	Leu	Phe	Leu	Arg	Ala	Phe	Thr	Asp	Phe	Leu	Ala	Phe	340	345	350	
Met	Val	Leu	Phe	Asn	Tyr	Ile	Ile	Pro	Val	Ser	Met	Tyr	Val	Thr	Val	355	360	365	
Glu	Met	Gln	Lys	Phe	Leu	Gly	Ser	Tyr	Phe	Ile	Thr	Trp	Asp	Glu	Asp	370	375	380	
Met	Phe	Asp	Glu	Glu	Met	Gly	Glu	Gly	Pro	Leu	Val	Asn	Thr	Ser	Asp	385	390	395	400
Leu	Asn	Glu	Glu	Leu	Gly	Gln	Val	Glu	Tyr	Ile	Phe	Thr	Asp	Lys	Thr	405	410	415	
Gly	Thr	Leu	Thr	Glu	Asn	Asn	Met	Ala	Phe	Lys	Glu	Cys	Cys	Ile	Glu	420	425	430	
Gly	His	Val	Tyr	Val	Pro	His	Val	Ile	Cys	Asn	Gly	Gln	Val	Leu	Pro	435	440	445	
Asp	Ser	Ser	Gly	Ile	Asp	Met	Ile	Asp	Ser	Ser	Pro	Gly	Val	Cys	Gly	450	455	460	
Arg	Glu	Arg	Glu	Glu	Leu	Phe	Phe	Arg	Ala	Ile	Cys	Leu	Cys	His	Thr	465	470	475	480
Val	Gln	Val	Lys	Asp	Asp	His	Cys	Gly	Asp	Asp	Val	Asp	Gly	Pro	Gln	485	490	495	
Lys	Ser	Pro	Asp	Ala	Lys	Ser	Cys	Val	Tyr	Ile	Ser	Ser	Ser	Pro	Asp	500	505	510	
Glu	Val	Ala	Leu	Val	Glu	Gly	Val	Gln	Arg	Leu	Gly	Phe	Thr	Tyr	Leu	515	520	525	
Arg	Leu	Lys	Asp	Asn	Tyr	Met	Glu	Ile	Leu	Asn	Arg	Glu	Asn	Asp	Ile	530	535	540	
Glu	Arg	Phe	Glu	Leu	Leu	Glu	Val	Leu	Thr	Phe	Asp	Ser	Val	Arg	Arg	545	550	555	560
Arg	Met	Ser	Val	Ile	Val	Lys	Ser	Thr	Thr	Gly	Glu	Ile	Tyr	Leu	Phe	565	570	575	
Cys	Lys	Gly	Ala	Asp	Ser	Ser	Ile	Phe	Pro	Arg	Val	Ile	Glu	Gly	Lys	580	585	590	
Val	Asp	Gln	Val	Arg	Ser	Arg	Val	Glu	Arg	Asn	Ala	Val	Glu	Gly	Leu	595	600	605	
Arg	Thr	Leu	Cys	Val	Ala	Tyr	Lys	Arg	Leu	Glu	Pro	Glu	Gln	Tyr	Glu	610	615	620	
Asp	Ala	Cys	Arg	Leu	Leu	Gln	Ser	Ala	Lys	Val	Ala	Leu	Gln	Asp	Arg	625	630	635	640
Glu	Lys	Lys	Leu	Ala	Glu	Ala	Tyr	Glu	Gln	Ile	Glu	Lys	Asp	Leu	Val	645	650	655	
Leu	Leu	Gly	Ala	Thr	Ala	Val	Glu	Asp	Arg	Leu	Gln	Glu	Lys	Ala	Ala	660	665	670	
Asp	Thr	Ile	Glu	Ala	Leu	Gln	Lys	Ala	Gly	Ile	Lys	Val	Trp	Val	Leu	675	680	685	
Thr	Gly	Asp	Lys	Met	Glu	Thr	Ala	Ser	Ala	Thr	Cys	Tyr	Ala	Cys	Lys	690	695	700	
Leu	Phe	Arg	Arg	Ser	Thr	Gln	Leu	Leu	Glu	Leu	Thr	Thr	Lys	Lys	Leu				

705 710 715 720
 Glu Glu Gln Ser Leu His Asp Val Leu Phe Asp Leu Ser Lys Thr Val
 725 730 735
 Leu Arg Cys Ser Gly Ser Met Thr Arg Asp Ser Phe Ser Gly Leu Ser
 740 745 750
 Thr Asp Met His Asp Tyr Gly Leu Ile Ile Asp Gly Ala Ala Leu Ser
 755 760 765
 Leu Ile Met Lys Pro Arg Glu Asp Gly Ser Ser Ser Gly Asn Tyr Arg
 770 775 780
 Glu Leu Phe Leu Glu Ile Cys Arg Asn Cys Ser Ala Val Leu Cys Cys
 785 790 795 800
 Arg Met Ala Pro Leu Gln Lys Ala Gln Ile Val Lys Leu Ile Lys Phe
 805 810 815
 Ser Lys Glu His Pro Ile Thr Leu Ala Ile Gly Asp Gly Ala Asn Asp
 820 825 830
 Val Ser Met Ile Leu Glu Ala His Val Gly Ile Gly Val Ile Gly Lys
 835 840 845
 Glu Gly Arg Gln Ala Ala Arg Asn Ser Asp Tyr Ala Ile Pro Lys Phe
 850 855 860
 Lys His Leu Lys Lys Met Leu Leu Val His Gly His Phe Tyr Tyr Ile
 865 870 875 880
 Arg Ile Ser Glu Leu Val Gln Tyr Phe Phe Tyr Lys Asn Val Cys Phe
 885 890 895
 Ile Phe Pro Gln Phe Leu Tyr Gln Phe Phe Cys Gly Phe Ser Gln Gln
 900 905 910
 Thr Leu Tyr Asp Thr Ala Tyr Leu Thr Leu Tyr Asn Ile Ser Phe Thr
 915 920 925
 Ser Leu Pro Ile Leu Leu Tyr Ser Leu Met Glu Gln His Val Gly Ile
 930 935 940
 Asp Val Leu Lys Arg Asp Pro Thr Leu Tyr Arg Asp Ile Ala Lys Asn
 945 950 955 960
 Ala Leu Leu Arg Trp Arg Val Phe Ile Tyr Trp Thr Phe Leu Gly Val
 965 970 975
 Phe Asp Ala Leu Val Phe Phe Phe Gly Ala Tyr Phe Ile Phe Glu Asn
 980 985 990
 Thr Thr Val Thr Ile Asn Gly Gln Met Phe Gly Asn Trp Thr Phe Gly
 995 1000 1005
 Thr Leu Val Phe Thr Val Met Val Leu Thr Val Thr Leu Lys Leu Ala
 1010 1015 1020
 Leu Asp Thr His Tyr Trp Thr Trp Ile Asn His Phe Val Ile Trp Gly
 1025 1030 1035 1040
 Ser Leu Leu Phe Tyr Ile Ala Phe Ser Leu Leu Trp Gly Gly Val Ile
 1045 1050 1055
 Trp Pro Phe Leu Ser Tyr Gln Arg Met Tyr Tyr Val Phe Ile Ser Met
 1060 1065 1070
 Leu Ser Ser Gly Pro Ala Trp Leu Gly Ile Ile Leu Leu Val Thr Val
 1075 1080 1085
 Gly Leu Leu Pro Asp Val Leu Lys Lys Val Leu Cys Arg Gln Leu Trp
 1090 1095 1100
 Pro Thr Ala Thr Glu Arg Thr Gln Asn Ile Gln His Gln Asp Ser Ile
 1105 1110 1115 1120
 Ser Glu Phe Thr Pro Leu Ala Ser Leu Pro Ser Trp Gly Ala Gln Gly
 1125 1130 1135
 Ser Arg Leu Leu Ala Ala Gln Cys Ser Ser Pro Ser Gly Arg Val Val
 1140 1145 1150
 Cys Ser Arg Trp Glu Ser Glu Glu Cys Pro Val Leu Pro Leu His Pro
 1155 1160 1165
 Gly Leu Pro His Lys Ala Arg Tyr Gly Cys Cys Arg Ser Ser Leu Glu
 1170 1175 1180
 Met Pro Thr
 1185

1185
 1180
 1175
 1170
 1165
 1160
 1155
 1150
 1145
 1140
 1135
 1130
 1125
 1120
 1115
 1110
 1105
 1100
 1095
 1090
 1085
 1080
 1075
 1070
 1065
 1060
 1055
 1050
 1045
 1040
 1035
 1030
 1025
 1020
 1015
 1010
 1005
 1000
 995
 990
 985
 980
 975
 970
 965
 960
 955
 950
 945
 940
 935
 930
 925
 920
 915
 910
 905
 900
 895
 890
 885
 880
 875
 870
 865
 860
 855
 850
 845
 840
 835
 830
 825
 820
 815
 810
 805
 800
 795
 790
 785
 780
 775
 770
 765
 760
 755
 750
 745
 740
 735
 730
 725
 720
 715
 710
 705

<210> 35
 <211> 1508
 <212> PRT
 <213> Mus musculus

<400> 35

Met	Glu	Arg	Glu	Leu	Pro	Ala	Ala	Glu	Glu	Ser	Ala	Ser	Ser	Gly	Trp
1				5					10					15	
Arg	Arg	Pro	Arg	Arg	Arg	Arg	Trp	Glu	Gly	Arg	Thr	Arg	Thr	Val	Arg
		20						25					30		
Ser	Asn	Leu	Leu	Pro	Pro	Leu	Gly	Thr	Glu	Asp	Ser	Thr	Ile	Gly	Ala
	35						40					45			
Pro	Lys	Gly	Glu	Arg	Leu	Leu	Met	Arg	Gly	Cys	Ile	Gln	His	Leu	Ala
	50					55					60				
Asp	Asn	Arg	Leu	Lys	Thr	Thr	Lys	Tyr	Thr	Leu	Leu	Ser	Phe	Leu	Pro
65					70					75					80
Lys	Asn	Leu	Phe	Glu	Gln	Phe	His	Arg	Leu	Ala	Asn	Val	Tyr	Phe	Val
				85					90					95	
Phe	Ile	Ala	Leu	Leu	Asn	Phe	Val	Pro	Ala	Val	Asn	Ala	Phe	Gln	Pro
		100						105					110		
Gly	Leu	Ala	Leu	Ala	Pro	Val	Leu	Phe	Ile	Leu	Ala	Val	Thr	Ala	Ile
	115						120					125			
Lys	Asp	Leu	Trp	Glu	Asp	Tyr	Ser	Arg	His	Arg	Ser	Asp	His	Glu	Ile
	130					135					140				
Asn	His	Leu	Gly	Cys	Leu	Val	Phe	Ser	Arg	Glu	Glu	Lys	Lys	Tyr	Val
145					150					155					160
Asn	Arg	Tyr	Trp	Lys	Glu	Ile	Arg	Val	Gly	Asp	Phe	Val	Arg	Leu	Cys
				165					170					175	
Cys	Asn	Glu	Ile	Ile	Pro	Ala	Asp	Ile	Leu	Leu	Leu	Ser	Ser	Ser	Asp
		180						185						190	
Pro	Asp	Gly	Leu	Cys	His	Ile	Glu	Thr	Ala	Asn	Leu	Asp	Gly	Glu	Thr
	195						200					205			
Asn	Leu	Lys	Arg	Arg	Gln	Val	Val	Arg	Gly	Phe	Ser	Glu	Leu	Val	Ser
	210				215						220				
Glu	Phe	Asn	Pro	Leu	Thr	Phe	Thr	Ser	Val	Ile	Glu	Cys	Glu	Lys	Pro
225					230					235					240
Asn	Asn	Asp	Leu	Ser	Arg	Phe	Arg	Gly	Tyr	Ile	Met	His	Ser	Asn	Gly
			245						250					255	
Glu	Lys	Ala	Gly	Leu	His	Lys	Glu	Asn	Leu	Leu	Leu	Arg	Gly	Cys	Thr
		260						265					270		
Ile	Arg	Asn	Thr	Glu	Ala	Val	Ala	Gly	Ile	Val	Ile	Tyr	Ala	Gly	His
	275						280					285			
Glu	Thr	Lys	Ala	Leu	Leu	Asn	Asn	Ser	Gly	Pro	Arg	Tyr	Lys	Arg	Ser
	290					295				300					
Gln	Leu	Glu	Arg	Gln	Met	Asn	Cys	Asp	Val	Leu	Trp	Cys	Val	Leu	Leu
305					310					315					320
Leu	Val	Cys	Ile	Ser	Leu	Phe	Ser	Ala	Val	Gly	His	Gly	Leu	Trp	Val
			325						330					335	
Arg	Arg	Tyr	Gln	Glu	Lys	Lys	Ala	Leu	Phe	Asp	Val	Pro	Glu	Ser	Asp
		340						345					350		
Gly	Ser	Ser	Leu	Ser	Pro	Ala	Thr	Ala	Ala	Val	Tyr	Ser	Phe	Phe	Thr
	355						360					365			
Met	Ile	Ile	Val	Leu	Gln	Val	Leu	Ile	Pro	Ile	Ser	Leu	Tyr	Val	Ser
	370					375					380				
Ile	Glu	Ile	Val	Lys	Val	Cys	Gln	Val	Tyr	Phe	Ile	Asn	Gln	Asp	Ile
385				390						395					400
Glu	Leu	Tyr	Asp	Glu	Glu	Thr	Asp	Ser	Gln	Leu	Gln	Cys	Arg	Ala	Leu
			405						410					415	
Asn	Ile	Thr	Glu	Asp	Leu	Gly	Gln	Ile	Lys	Tyr	Ile	Phe	Ser	Asp	Lys

TOGETHER

Ile	His	Glu	Ser	Leu	Ser	Ile	Glu	Asn	Thr	Leu	Trp	Ala	Ser	Thr	Ile
		275					280					285			
Val	Ala	Ser	Gly	Thr	Val	Ile	Gly	Val	Val	Ile	Tyr	Thr	Gly	Lys	Glu
	290					295					300				
Thr	Arg	Ser	Val	Met	Asn	Thr	Ser	Asn	Pro	Asn	Asn	Lys	Val	Gly	Leu
305					310					315					320
Leu	Asp	Leu	Glu	Leu	Asn	Gln	Leu	Thr	Lys	Ala	Leu	Phe	Leu	Ala	Leu
				325					330					335	
Val	Val	Leu	Ser	Val	Val	Met,	Val	Thr	Leu	Gln	Gly	Phe	Ala	Gly	Pro
			340					345					350		
Trp	Tyr	Arg	Asn	Leu	Phe	Arg	Phe	Leu	Leu	Leu	Phe	Ser	Tyr	Ile	Ile
		355					360					365			
Pro	Ile	Ser	Leu	Arg	Val	Asn	Leu	Asp	Met	Gly	Lys	Ala	Ala	Tyr	Gly
	370					375					380				
Trp	Met	Ile	Met	Lys	Asp	Glu	Asn	Ile	Pro	Gly	Thr	Val	Val	Arg	Thr
385					390					395					400
Ser	Thr	Ile	Pro	Glu	Glu	Leu	Gly	Arg	Leu	Val	Tyr	Leu	Leu	Thr	Asp
				405					410					415	
Lys	Thr	Gly	Thr	Leu	Thr	Gln	Asn	Glu	Met	Val	Phe	Lys	Arg	Leu	His
			420					425					430		
Leu	Gly	Thr	Val	Ser	Tyr	Gly	Thr	Asp	Thr	Met	Asp	Glu	Ile	Gln	Ser
		435					440					445			
His	Val	Leu	Asn	Ser	Tyr	Leu	Gln	Val	His	Ser	Gln	Pro	Ser	Gly	His
	450					455					460				
Asn	Pro	Ser	Ser	Ala	Pro	Leu	Arg	Arg	Ser	Gln	Ser	Ser	Thr	Pro	Lys
465					470					475					480
Val	Lys	Lys	Ser	Val	Ser	Ser	Arg	Ile	His	Glu	Ala	Val	Lys	Ala	Ile
				485					490					495	
Ala	Leu	Cys	His	Asn	Val	Thr	Pro	Val	Tyr	Glu	Ala	Arg	Ala	Gly	Ile
			500					505					510		
Thr	Gly	Glu	Thr	Glu	Phe	Ala	Glu	Ala	Asp	Gln	Asp	Phe	Ser	Asp	Glu
		515					520					525			
Asn	Arg	Thr	Tyr	Gln	Ala	Ser	Ser	Pro	Asp	Glu	Val	Ala	Leu	Val	Arg
	530					535					540				
Trp	Thr	Glu	Ser	Val	Gly	Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Ala	Ser
545					550					555					560
Met	Gln	Leu	Lys	Thr	Pro	Ser	Gly	Gln	Val	Leu	Thr	Tyr	Cys	Ile	Leu
				565					570					575	
Gln	Met	Phe	Pro	Phe	Thr	Ser	Glu	Ser	Lys	Arg	Met	Gly	Ile	Ile	Val
			580					585					590		
Arg	Asp	Glu	Ser	Thr	Ala	Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp
		595					600					605			
Val	Ala	Met	Ser	Thr	Ile	Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu
	610					615									

```

Leu Asn Ala Phe Arg Arg Lys His Asp Cys Ala Leu Val Ile Ser Gly
  755          760          765
Asp Ser Leu Glu Val Cys Leu Arg Tyr Tyr Glu His Glu Leu Val Glu
  770          775          780
Leu Ala Cys Gln Cys Pro Ala Val Val Cys Cys Arg Cys Ser Pro Thr
  785          790          795          800
Xaa Lys Ala His Ile Val Thr Leu Leu Arg Gln His Thr Arg Lys Arg
          805          810          815
Thr Cys Ala Ile Gly Asp Gly Gly Asn Asp Val Ser Met Ile Gln Ala
          820          825          830
Ala Asp Cys Gly Ile Gly Ile Glu Gly Lys Glu Gly Lys Gln Ala Ser
          835          840          845
Leu Ala Ala Asp Phe Ser Ile Thr Gln Phe Arg His Ile Gly Arg Leu
          850          855          860
Leu Met Val His Gly Arg Asn Ser Tyr Lys Arg Ser Ala Ala Leu Gly
          865          870          875          880
Gln Phe Val Met His Arg Gly Leu Ile Ile Ser Thr Met Gln Ala Val
          885          890          895
Phe Ser Ser Val Phe Tyr Phe Ala Ser Val Pro Leu Tyr Gln Gly Phe
          900          905          910
Leu Met Val Gly Tyr Ala Thr Ile Tyr Thr Met Phe Pro Val Phe Ser
          915          920          925
Leu Val Leu Asp Gln Asp Val Lys Pro Glu Met Ala Ile Leu Tyr Pro
          930          935          940
Glu Leu Tyr Lys Asp Leu Thr Lys Gly Arg Ser Leu Ser Phe Lys Thr
          945          950          955          960
Phe Leu Ile Trp Val Leu Ile Ser Ile Tyr Gln Gly Gly Ile Leu Met
          965          970          975
Tyr Gly Ala Leu Leu Phe Glu Asp Glu Phe Val His Val Val Ala
          980          985          990
Ile Ser Phe Thr Ala Leu Ile Leu Thr Glu Leu Leu Xaa Val Ala Leu
          995          1000          1005
Thr Ile Arg Thr Trp His Trp Leu Met Val Val Ala Glu Phe Leu Ser
          1010          1015          1020
Leu Gly Cys Tyr Val Ala Ser Leu Ala Phe Leu Asn Glu Tyr Phe Gly
          1025          1030          1035          1040
Ile Gly Arg Val Ser Phe Gly Ala Phe Leu Asp Val Ala Phe Ile Thr
          1045          1050          1055
Thr Val Thr Phe Leu Trp Lys Val Ser Ala Ile Thr Val Val Ser Cys
          1060          1065          1070
Leu Pro Leu Tyr Val Leu Lys Tyr Leu Lys Arg Lys Leu Ser Pro Pro
          1075          1080          1085
Ser Tyr Ser Lys Leu Ser Ser
          1090          1095

```

<210> 37

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> domain

<220>

<221> VARIANT

<222> (1)

<223> Xaa = Asp, Asn, or Ser

<220>

<221> VARIANT

<222> (2)
<223> Xaa = Gln, Glu, Asn, or Arg

<220>
<221> VARIANT
<222> (3)
<223> Xaa = Ser or Ala

<220>
<221> VARIANT
<222> (4)
<223> Xaa = Leu, Ile, Val, Ser, Ala, or Asn

<220>
<221> VARIANT
<222> (5)
<223> Xaa = Leu, Ile, or Val

<220>
<221> VARIANT
<222> (6)
<223> Xaa = Thr, Ser, or Asn

<220>
<221> VARIANT
<222> (9)
<223> Xaa = Ser or Asn

<400> 37
Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu Xaa
1 5

<210> 38
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> domain

<220>
<221> VARIANT
<222> (1)
<223> Xaa = Leu, Ile, or Val

<220>
<221> VARIANT
<222> (2)
<223> Xaa = Cys, Ala, Met, or Leu

<220>
<221> VARIANT
<222> (3)
<223> Xaa = Ser, Thr, Phe, or Leu

<220>
<221> VARIANT
<222> (9)
<223> Xaa = Leu or Ile

<400> 38

Xaa Xaa Xaa Asp Lys Thr Gly Thr Xaa Thr
 1 5 10

<210> 39

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> domain

<220>

<221> VARIANT

<222> (1)

<223> Xaa = Thr, Ile, or Val

<220>

<221> VARIANT

<222> (5)

<223> Xaa = any amino acid

<220>

<221> VARIANT

<222> (8)

<223> Xaa = Ala, Ser, or Gly

<220>

<221> VARIANT

<222> (10)

<223> Xaa = Ala, Ser, or Val

<400> 39

Xaa Gly Asp Gly Xaa Asn Asp Xaa Pro Xaa Leu
 1 5 10

<210> 40

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> domain

<220>

<221> VARIANT

<222> (6)

<223> Xaa = Leu, Ile, Val, or Met

<220>

<221> VARIANT

<222> (7)

<223> Xaa = Thr or Ile

<400> 40

Asp Lys Thr Gly Thr Xaa Xaa
 1 5

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000